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(71) Applicant (for all designated States except US): DEVGEN N.V. [BE/BE]; Technologiepark Zwijnaarde 9, B-9052 Zwijnaarde (BE).

(72) Inventors; and

(75) Inventors/Applicants (for US only): SMITS, Elke [BE/BE]; Devgen n.v., Technologiepark Zwijnaarde 9, B-9052 Zwijnaarde (BE). VAN CRIEKINGE, Wim, Maria, Rene [BE/BE]; Pastoriestaat 17, B-2500 Kontich (BE). BOGAERT, Thierry, Andre, Oliver, Eddy [BE/BE]; Wolvendreed 26g, B-8500 Kortrijk (BE).

(74) Agents: BALDOCK, Sharon, Claire et al.; Boult Wade Tennant, 27 Furnival Street, London EC4A 1PQ (GB).

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(54) Title: PHAGOCYTIC ASSAY METHOD

(57) Abstract

The invention provides assay methods for determining whether a compound is an enhancer or an inhibitor of a signal transduction pathway which promotes phagocytosis of apoptotic cells. The methods involve exposing a phagocytic cell to apoptotic cells, optionally transfected with a reporter gene, and measuring the extent of phagocytosis in the presence or absence of the test compound. Expression vectors are provided to transfect mammalian cells with DNA sequences which when expressed influence the rate of phagocytosis of apoptotic cells such as the human homologue of the *C. elegans* ced-6 gene.

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PHAGOCYTIC ASSAY METHOD

The present invention relates to the field of programmed cell death or apoptosis and in particular to the phenomenon whereby apoptotic cells are rapidly phagocytosed or engulfed by other cells.

Specifically, the invention provides assays and materials for use therein, which measure phagocytosis of apoptotic cells. Such assays can be used to identify chemical substances which influence the phagocytic uptake of apoptotic cells and have potential pharmacological activity. The assays of the invention are well adapted for medium-and high—throughput screening using a multi-well plate format.

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During development and maintenance of living tissues a large number of cells undergo programmed cell death or apoptosis. This is observed in both vertebrates and invertebrates. For example, it has been shown that in the nematode C. elegans 131 cells undergo programmed cell death (Lui and Hengartner (1997) early 1997 International Worm Meeting, Abstract 371). Lysis of the apoptotic cells is potentially harmful since their contents may cause toxic damage to the surrounding It has been observed that this harmful effect is avoided because apoptotic cells are engulfed and subsequently degraded by other cells. In mammals the engulfing cells may be professional or semiprofessional phagocytes such as neutrophils or macrophages or they may be neighbours of the dying cells.

A key feature of the process of programmed cell death, or apoptosis, is the efficiency with which the dying cells are recognized and engulfed by phagocytes (Savill, J.et. al, Immunol Today, 14:131-136, 1993.).

Apoptosis triggers a distinct sequence of events

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characterized by the expression of phosphatidylserine on the cell surface, DNA fragmentation or laddering and the release of membrane-bound cell fragments called apoptotic blebs and bodies (Cohen, J. J.et. al, 5 Annu Rev Immunol, 10:267-293, 1992.; Kerr J.F.R.et. al, Br J Cancer, 26:239, 1972.). Apoptotic cells and bodies are phagocytosed via various receptors that recognize phosphatitdylserine and other undefined ligands unique to the surface of apoptotic material (Savill, J. S.et. al, J Clin Invest, 83:865-875, 10 1989.; Fadok, V. A.et. al, J Immunol, 148:2207-2216, 1992.; Savill, J.et. al, Nature, 343:170-173, 1990.). In this way, apoptotic cells, which contain potentially inflammatory factors, are rapidly cleared by neighboring cells acting as semi-professional 15 phagocytes or voracious experts of the macrophage line without inducing an inflammatory response (Fadok, V. A.et. al, J Clin Invest, 101:890-898, 1998.).

The process of apoptosis has been associated with a number of human diseases, including cancer, autoimmune diseases, various neurodegenerative diseases, such as Amyotrophic Lateral Sclerosis, Huntingdon's disease and Alzheimer's disease, stroke, myocardial infarction and AIDS (Thompson, CB, Science 267, pp 1456-1462). Thus, much attention has been focused on elucidating the mechanism of apoptosis and the genes controlling it with a view to developing new therapeutic strategies for these diseases.

Particular diseases have been associated with an impairment of phagocytosis of apoptotic bodies. Examples of such diseases include autoimmune diseases such as systemic lupus erythematosus, (Herrmann, M.et. al, Arthritis Rheum, 41:1241-1250, 1998.), AIDS (Zocchi, M. R.et. al, AIDS, 11:1227-1235, 1997.),

acute pulmonary infections (Cox, G.et. al, Am.J

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Respir.Cell Mol.Biol., 12:232-237, 1995.) and allergy (Ying, S.et. al, Proc Assoc Am Physicians, 109:42-50, 1997.). It is clear that modulation of phagocytosis of apoptotic cells by drugs is a promising strategy for future therapies.

Phagocytosis of apoptotic cells in vertebrates has been observed to be a very complicated process and how any signal generated by the dying cell is received and transduced by the engulfing cell is not understood.

A swift engulfment of apoptotic cells is observed in the hermaphrodite C. elegans and this worm has provided a useful tool for study of the engulfment process. For example, six genes have been identified in C. elegans as effecting engulfment known as ced-1, ced-2, ced-5, ced-6, ced-7 and ced-10. Of these ced-6 has been singled out by the present inventors for particular study. It is known that ced-6 maps to chromosome III near daf-4 in C. elegans (Lui and Hengartner (1997); Lui and Hengartner (1996) East Coast Worm Meeting Abstract 128). That work showed that two cosmids from this region, F56D2 and F43F12 could rescue C. elegans with a ced-6 (n1813) engulfment defect. A 10 kb Xho I subclone from F56D2 with rescuing activity was identified as carrying the ced-6 gene.

The present inventors have identified two human homologues of the *C. elegans* ced-6 (h1ced-6 and h2ced-6), h2ced-6 being a splice variant of h1ced-6 and thought to be a dominant negative version thereof. Both homologues have been shown to be present in the human cell-line THP-1. A surprising degree of sequence homology between hCED-6 and *C. elegans* CED-6 has been found. hCED-6 has a phosphotyrosine binding domain from about amino acid position 11 to about

amino acid position 190 as shown in Figure 4 suggesting its involvement in a tyrosine kinase signal transduction pathway.

hlCED-6 and h2CED-6 proteins and their encoding nucleic acids are useful for carrying out assays as described herein to identify compounds which are inhibitors or enhancers of a signal transduction pathway which promotes phagocytosis of apoptotic cells. In particular they are useful for identifying inhibitors or enhancers of h1CED-6 and h2CED-6 or inhibitors or enhancers of the transcription thereof. Such inhibitors or enhancers may be useful therapeutic agents in the treatment of some of the aforementioned diseases.

In accordance with its first aspect the invention provides an expression vector capable of expressing h1CED-6 or h2CED-6 which vector comprises a sequence of deoxynucleotides encoding the amino acid sequence of Figure 4 or Figure 5 or an amino acid sequence which differs from the amino acid sequence of Figure 4 or Figure 5 only in amino acid changes which are conservative of biological function.

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The term "biological function" is defined herein to mean the ability to regulate or affect phagocytosis of apoptotic cells. Amino acid changes which are "conservative" are those which permit biological function to be retained although it may be less than or greater than the level of biological function of the wild-type human CED-6 protein. Such conservative changes may include insertion or deletion of one or more amino acids or substitution of one or more amino acids with another amino acid or acids having similar chemical characteristics. The choice of amino acids for making conservative changes will be well-known to

those skilled in the art.

In a preferred embodiment the expression vector is one comprising the sequence of deoxynucleotides shown from the transcription start codon to the transcription stop codon shown in Figure 2 or Figure 3 and optionally a vector comprising the sequence of deoxynucleotides shown in Figure 2 or Figure 3.

In a particularly preferred embodiment the expression 10 vector of the invention comprises a sequence of nucleotides encoding a reporter gene positioned so that expression of h1CED-6 or h2CED-6 results in expression of the reporter gene. The reporter gene 15 may be positioned 3' or 5' to said hlced-6 or h2ced-6 and may be expressed as a fusion protein with h1CED-6 or h2CED-6. Suitable reporter genes are those which express a fluorescent product such as green fluorescent protein (GFP). Other suitable reporter genes are enzymes, such as \$-galactosidase or 20 luciferase, which are capable of acting on a substrate to produce a detectable product, for example a -fluorescent product or luminescent product. Examples of expression vectors in accordance with the invention are pGA3103 and pGA3104 which are shown in Figures 29 25 and 10 respectively.

In another preferred embodiment the expression vector of the invention expresses an epitope tag at the amino and/or carboxy terminal of the h1CED-6 or h2CED-6 protein. An example is the plasmid pBAD/HisA-h1ced-6 the DNA sequence of which is shown in Figure 17.

It will be understood that the expression vectors

described above will comprise not only nucleic acid
encoding h1CED-6 or h2CED-6 or functional variants
thereof but also regulatory sequences operably linked

to said nucleic acid, such as promoter regions that are capable of effecting expression of the DNA fragments. The term "operably linked" refers to a juxtaposition wherein the components described are in a relationship permitting them to function in their intended manner.

Regulatory elements required for expression include promoter sequences to bind RNA polymerase and to 10 direct an appropriate level of transcription initiation and also translation initiation sequences for ribosome binding. For example, a bacterial expression vector may include a promoter such as the lac promoter and for translation initiation the Shine-Dalgarno sequence and the start codon AUG. Similarly, 15 a eukaryotic expression vector may include a heterologous or homologous promoter for RNA polymerase II, a downstream polyadenylation signal, the start codon AUG, and a termination codon for detachment of the ribosome. Such vectors may be obtained 20 commercially or be assembled from the sequences described by methods well known in the art. Promoter sequences which may be used in the expression vectors of the invention include & HSP, CMV, SV40, EF-1α, UbC, SG, RSV, TRE/minCMV, HSV TK, 5', LTR and 25 QBISP136 enhanced CMV.

Examples of expression vectors described herein are plasmids but may also be virus or phage vectors. Such vectors will normally possess an origin of replication and one or more selectable markers such as a gene for antibiotic resistance. It is particularly preferred that the expression vectors of the invention are suitable for transfection of mammalian cells and therefore may be provided with a selectable marker accordingly.

In accordance with a second aspect the invention provides a mammalian cell-line transfected with any of the expression vectors described above. Methods of transfecting mammalian cells are well-known to those 5 skilled in the art. The cell-line may be one which is capable of growing in monolayer culture or in suspension culture. Suitable cell-lines are fibroblast cell-lines or epithelial cell-lines such as COS1, BHK21, L929, pc12, CV1, SWISS3T3, HT144, IMR32, 10 ... HEPG2, MDCK, MCF7, 293, Hela, A549, SW48 or G361. Primary cell-lines such as human dermal FIBs, dermal kératinocytes, leucocytes, monocytes, lyphocytes, dendritic cells or macrophages may also be used. Particularly preferred for use in the phagocytosis assays of the invention are mammalian professional or semi-professional phagocytes of which examples are mouse macrophage cell-line J774 or human monocyte cell-line THP1 which has been shown to express h1CED-6 and h2CED-6 (see Example 3 and Figure 6). Both of the above cell-lines may be referred to as monocyte celllines since monocytes are capable of differentiating into macrophages which is the form in which they are used for the assay of the invention.

In accordance with a third aspect the invention provides a method for determining whether a compound is an enhancer or an inhibitor of a signal transduction pathway which promotes phagocytosis of apoptotic cells which method comprises exposing

mammalian cells transfected with h1ced-6 or h2ced-6 as described above to apoptotic particles and measuring the rate of phagocytic uptake of said particles by said transfected cells in the presence or absence of said compound. The test compound is preferably added prior to addition of said apoptotic particles.

Suitable apoptotic particles are cells such as

neutrophils, lymphocytes, erythrocytes, lymphocytes or dendritic cells which have been rendered apoptotic and are optionally opsonized by exposure to serum. Cells suitable for forming the apoptotic particles include the cell-lines L929 and PC12. A particularly 5 preferred cell-line for use as an apoptotic particle is the growth factor dependent mouse cell-line Ba/F3. These may be grown in standard culture medium as described in Example 5 and can be rendered apoptotic by growth in the absence of the growth factor IL-3 for 10 a suitable period (for example about 20 hours) prior to use. The apoptotic status of the cells can be determined using, for example, an annexin/propidium iodide labelling kit available from Boeringher 15 Mannheim (Brussels, Belgium). Cells are considered early apoptotic if they are about 20% annexin positive and less than about 5% propidium iodide negative.

The PC 12 cell-line may be rendered apoptotic by growth in standard medium in the absence of nerve growth factor.

As an alternative to the cells described above the apoptotic particles could be a non-living material such as dye-labelled latex beads. 0.1µM, 1µM, 4µM and 10µM beads that have either an amino or carboxylate group are available from Sigma-Aldrich, Bornem, Belgium, or Molecular Probes, Eugene, USA.

In order for the assay described to be suitable for high-throughout compound screening it is preferred that the apoptotic particles bear some kind of detectable label so that it will be readily apparent that the particles have been taken up by the transfected mammalian cell and so that this can be quantified. The inventors have found that this may be easily achieved by stably transfecting the cells

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comprising the apoptotic particles with an expression vector comprising a reporter gene. A particularly suitable reporter gene encodes to be β -galactosidase which is capable of cleaving the fluorogenic substrate fluorescein di-b-D-galactopyranoide to a fluorescent compound which may be monitored using standard fluorescence detection equipment. Other fluorescent substrates are available for \beta-galactosidase. A plasmid pcDNA3.1/HIS/lacz, which expresses βgalactosidase and is suitable for transfecting cells used as apoptotic particles, for example Ba/F3, is shown in Figure 11. Other suitable reporter genes are those encoding fluorescent proteins such as green fluorescent protein or proteins capable of generating a luminescent signal such as luciferase. Plasmids, pEGFP-N3 or PEGFP-C2, available from Clontech, are suitable for transfecting cells used as apoptotic particles with GFP and are shown in Figures 7, 8, 26 and 27. A plasmid "PGL Control" available from Promega is suitable for transfecting cells to be used as apoptotic particles such as Ba/F3 cells with a gene encoding luciferase. The DNA sequence of "PGL control" is shown in Figure 19.

It will be appreciated that the choice of reporter gene for the apoptotic particles may be governed by the presence of any reporter gene in the transfected mammalian cells. For example, the presence of the same reporter gene in the transected mammalian cells transfected with h1 or h2 ced-6 and the apoptotic cells is not prima facie desirable because of overlap of signals, although this may not always be the case.

It will further be appreciated that a wide variety of compounds can be tested to see whether they are inhibitors or enhancers of signal transduction pathways which promote phagocytosis of apoptotic

- cells. The compound may be of any chemical formula, a polymer or a monomer. For example the test compound may be genomic DNA, cDNA, RNA, PNA, a protein or polypeptide, an amino acid, nucleoside or nucleotide.
- The compound may be one of known biological or pharmacological activity, a known compound without such activity or a novel molecule such as might be present in a combinatorial library of compounds.
- It will be appreciate that where any compound the presence of which results in no or a decreased amount of engulfment of apoptotic particles by the transfected mammalian cells, those cells must be tested for viability. The presence of viable cells will confirm that lack of engulfment is due to the effect of the test compound on phagocytic activity and not just non-specific toxicity.
- Furthermore, any compound identified as an inhibitor or an enhancer of phagocytosis of apoptotic cells by 20 the assay described above will be further tested to establish whether the effect is medicated through CED-6. In the case of a compound identified as an enhancer of phagocytosis of apoptotic cells this can 25 be achieved by carrying out a phagocytosis assay exactly as described above with mammalian cells which are not transfected with hlced-6 or h2ced-6. If the compound is able to induce a phenotype in the untransfected cells which is similar to the phenotype of those cells when transfected with h1ced-6 then it is an indication that the compound in question exerts its effect via CED-6 or via the CED-6 signal transduction pathway.
- Similarly, if a compound identified in the above described assay is an inhibitor of phagocytosis of apoptotic cells it can be confirmed whether its effect

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is via CED-6 or the CED-6 signal transduction pathway by examining the phenotype of the transfected mammalian cells exposed to the compound. Reversion to a wild-type phenotype is an indication of action via CED-6 or the CED-6 signal transduction pathway.

In a fourth of its aspects the invention provides a method for determining whether a compound is an inhibitor or an enhancer of a signal transduction pathway which promoter phagocytosis of apoptotic cells which method comprises the steps of:

- (1) micro-injecting into a mammalian cell a human CED-6 protein comprising the sequence of amino acids shown in Figure 4 or Figure 5 or a sequence of amino ids differing from that shown in Figure 4 or Figure 5 only in amino aid changes conservative of function, and
- (2) exposing the mammalian cell produced in step (1) to apoptotic particles and measuring the rate of phagocytic uptake of said particles by said cell in the presence and absence of said compound.

Preferably, the mammalian cell is micro-injected with a fusion protein comprising hlCED-6 or h2CED-6 and a reporter gene which may be any one of the reporter genes described above. Preferred fusion proteins are obtainable by expression from the GFP and h1ced-6 encoding sequences of the plasmids shown in Figures 9 or 28.

All of the preferred features and embodiments described above for assays with transfected mammalian cell-lines can be applied to cells micro-injected with

h1CED-6 or h2CED-6 or fusions thereof as described above.

In a fifth aspect the invention provides a method for determining whether a compound is an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells which method comprises the steps of:

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(1) micro-injecting or transfecting into a mammalian cell a vector expressing RNA antisense to all or a portion of the sequence of nucleotides shown in Figure 2 or Figure 3;

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(2) exposing the mammalian cell produced in step (1) to apoptotic particles and measuring the rate of phagocytic uptake of said particles by said cell in the presence or absence of said compound.

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Preferably, the antisense DNA comprises a sequence of nucleotides which is capable of hybridizing to a sequence of nucleotides as shown in Figure 2 or Figure 3 under conditions of stringency which are higher than 2xSSC; 0.1%SDS; 25°C to 50°C.

All of the preferred features and embodiments described above for assays with transfected mammalian cell lines can be applied to the cell-lines injected with antisense RNA.

It will be appreciated that the transfected mammalian cells for use in the assays described above may be transfected with hlced-6 or h2ced-6. Since h2ced-6 is thought to be a dominant negative version of h1ced-6 having an opposite biological effect, transfected

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cells can be chosen depending on whether it is desired to identify compounds which are inhibitors or enhancers of apoptotic cell phagocytosis. For example cells transfected with h1ced-6 would be particularly suitable for identifying inhibitors of phagocytosis of apoptotic cells while cells transfected with h2ced-6 would be particularly suitable for identifying enhancers.

It is hereby stated that the invention also relates to any compound identified as an inhibitor or enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells as identified in accordance with any of the assay methods described herein.

The nucleotide sequences for h1ced-6 and h2ced-6 are shown in Figures 2 and 3 respectively. In addition cDNAs encoding the alterative splice h2CED-6 and the insert to reconstitute h1ced-6 from h2ced-6 have been deposited at the Belgian Coordinated Collections of Microorganisms (BCCM) at Laboratorium voor Moleculaire biologie - plasmidencollective (LMBP) B 9000, Gent, Belgium in accordance with the Budapest Treaty on 8th June 1998 and hae been accorded the Accession Nos 3868 and 3869 respectively.

Sequences can be obtained in both deposits using T3 or T7 primers (either one or both can be used, they are at different sites of the actual insert). Both are commercially available from Clontech (~1227 and~1228) and sequence is shown below

T7 primer: 5' (TAATACGACTCACTATAGGGAGA) 3'

T3 primer: 5' (ATTAACCCTCACTAAAGGGA) 3'

In addition to developing assays based on mammalian cells which over or under express human CED-6 protein the present inventors have identified epitopes of h1CED-6 and have generated useful antibodies thereto.

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Therefore in a sixth aspect the invention comprises a fragment of human CED-6 protein having the amino acid sequence as shown in Figure 4 wherein said fragment includes the sequence of amino acids HRAFSRKKDKTC, FLGSTEVEQPKGTE or TRNGTQPPPVPSRST. Antibody preparations have been prepared which comprise antibodies to one or more of the above epitopes. Such antibody preparations are obtainable by the method described in Example 6 and their specificity is demonstrated by the Western Blots carried out in Example 7 (see Figures 20 to 25).

The antibodies described above may be used in a method of diagnosing a disease in a patient which is

20 associated with over or under expression of human CED6 in phagocytic cells. Specifically, there is provided a method for diagnosing a disease associated with the over or under expression of human CED-6 protein in phagocytic cells in an individual which comprises:

- (a) obtaining a sample of phagocytes from said individual;
- (b) exposing said phagocytes to an antibody preparation as described above;
 - (c) quantitatively measuring the presence of any immune complexes formed between said antibodies and said CED-6 protein; and
 - (d) comparing the amount of immune complex

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formed with that formed using phagocytes from a control individual.

- The antibodies described above may be further used in assays for determining whether a compound is an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells. Specifically, there is provided a method for determining whether a compound is an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells which method comprises:
- (a) exposing a mammalian cell transfected with an expression vector as described above to the compound to be tested;
 - (b) exposing said mammalian cell to an antibody preparation as described above;
 - (c) quantitatively measuring the presence of any immune complex formed between said antibodies and protein expressed by said cells; and
 - (d) comparing the level of immune complex detected with the amount of immune complex detected in a mammalian cell transfected as described in step (a) which has not been exposed to said compound.
- In the above described method the mammalian cell may be selected from COS1, BHK21, L929, CU1, SWISS 3T3, HT144, IMR32, HEPG2, MDCK, MCF7, 293, hela, A549, SW48 or G361 with COS1 cells being particularly preferred. Alternatively, the mammalian cell is a human dermal

FIB, dermal keractinocyte, leucocyte, monocyte, hyphocyte, dendritic cell or macrophage. Preferred are professional phagocytes such as mouse macrophage cell-line J774 or human monocyte cell-line THP-1.

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Other uses for the antibodies of the inventions include purification of h1CED-6 and identification of proteins interacting with CED-6 so that the signal transduction pathway can be characterised, detecting over or under expression, cellular localization or post-translational modifications of hCED-6, epitope mapping and identification of active sites and pharmaceutical compositions comprising said antibodies in a suitable carrier or diluent.

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In accordance with a seventh aspect the invention also provides a method for diagnosing a disease associated with the over- or under-expression of human CED-6 in phagocytic cells in an individual, which method comprises:

- (a) obtaining a sample of phagocytes from said individual,
- (b) isolating RNA from said phagocytes,
- (c) preparing cDNA from said RNA,

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- (d) performing a first PCR reaction on said cDNA,
- (e) performing a second (nested) PCR on the reaction product of said first PCR reaction,

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f) quantitatively and qualitatively measuring the presence of human ced-6 RNA by analysing the reaction products from the first and second PCR and

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(g) comparing the amount and type of reaction products formed in the first and second PCR with that of the reaction products formed using phagocytes from control individuals.

Preferably, the PCR is performed with primers derived from the sequence of h1ced-6 or h2ced-6 as defined herein or derived from the vector used in the generation of cDNA. In particular said first PCR may be performed with primers having nucleotide sequences:

- 1) cgcaaggatccccatgaaccgtgcttttagcaggaag
- 2) gatctactaggtactggag

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The second PCR may be performed with primers having nucleotide sequences:

- 1) cgcaaggatccccatgaaccgtgcttttagcaggaag
- 15 2) gcggatggtaccgtcgactgctgatacttgagttattctcag

The assay methods described herein, developed by the present inventors for determining whether compounds are enhancers or inhibitors of human CED-6 have been found to be more generally applicable for identifying compounds which influence phagocytosis of apoptotic cells by any mechanism, not necessarily related to human CED-6 or the signal transduction pathway of which it forms a component.

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Liu et al. (Liu, Y.et. al, The American Association of Immunologists, 1:1999.) describe an assay for identifying compounds which influence phagocytosis of apoptotic cells, in which varying concentrations of the compound to be tested are added to the phagocytes which are subsequently seeded with apoptotic cells. To quantify phagocytosis of apoptotic cells, the authors used a microscopic quantification of phagocytosis in which the uptake of apoptotic cells was shown by electron microscopy and counted by light microscopy with a minimum of cells per slide being counted (Savill, J. S.Wyllie, A. H.Henson, J. E.Walport, M.

J.Henson, P. M.Haslett, C., J Clin Invest, 83:865-875, 1989.).

The presently known techniques for quantitating the phagocytosis of apoptotic cells do not readily lend themselves to high throughput screening of compounds for potential pharmacological activity. This is largely because the known assay techniques rely on microscopic counting of the proportion of phagocytes which have ingested apoptotic cells when exposed to the test compound. However, the present assays overcome this drawback because they can be performed in the multi-well assay format and provide detection systems which do not involve microscopy.

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Thus, in accordance with a further aspect of the invention there is provided a method of identifying a compound which is an enhancer or inhibitor of phagocytosis of apoptotic cells which comprises:

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a) exposing a mammalian professional or semiprofessional phagocyte to an apoptotic mammalian cell
which has been stably transfected with a reporter gene
capable of generating a signal detectable without
microscopy, in the presence of absence of the compound
to be tested,

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b) removing any apoptotic cells which are not engulfed by said phagocytes and

c) detecting any signal of the reporter gene from said phagocytes;

wherein any difference in signal in the presence of said compound compared to the signal in the absence of said compound is an indication that said compound is an inhibitor or an enhancer of phagocytosis of

apoptotic cells.

Usually, in the above method it is preferable to incubate the phagocytic cells with the test compound prior to addition of the apoptotic cells. A suitable incubation time might be about 15 to 30 minutes.

Suitable phagocytic cells for carrying out the method of the invention are mouse J774 cells or human THP-1 cells as described elsewhere herein. These cells are monocyte cell-lines but are cultured so as to differentiate them into macrophages prior to addition of apoptotic cells.

15 The apoptotic cells for use in the above method may be apoptotic neutophils, apoptotic lymphocytes or apoptotic erythrocytes. The apoptotic cells may optionally be opsonised by exposure to serum.

Preferred apoptotic cells are the adherent cell-lines 20 L929 or PC12 and, in particular, the growth factor dependant mouse cell-line Ba/F3 described elsewhere herein.

The apoptotic cells are stably transfected with a 25 reporter gene of the types and using the methods described above. One particular problem which can arise with the use of reporter genes is that expression of the gene in an apoptotic cell, which is effectively dying, can be much less than in a fully viable cell. If viable cells are present amongst the 30 apoptotic particles added to the phagocytes and there is inadequate washing of the unphagocytosed particles the signal from the viable cells will mask any signal from the apoptotic phagocytosed cells. Athough it is possible to ensure that adequate washing occurs the 35 inventors have developed a particular embodiment where this problem is avoided.

Specifically, this involves using a reporter gene expressing a protein, preferably an enzyme, with a low turnover in the cell such that the living cell and the apoptotic particles have approximately the same protein concentration or enzymatic activity. This overcomes the drawbacks described above. Several possible reporter proteins and substrates have been described in Handbook of fluorescent probes and research chemicals, ed by P. Haugland (Molecular probes, Eugene, OR, USA) which may be used. However, 10 the inventors have found β -galactosidase (lacZ) to be particularly suitable. The enzyme has a relative slow turnover and it is shown that the cells and the apoptotic particles have relatively equal amounts of 15 activity. Furthermore several substrates exist for β galactosidase (see molecular probes, Eugene, OR, USA) from which the inventors have used FDG mentioned above. This makes it possible to develop a high throughput screen to select for compounds that alter 20 the phagocytosis of apoptotic particles.

The phagocytes for use in the method of the invention may by wild-type cells or they may be transgenic or mutant cells. A mutant cell may have reduced or increased phagocytic activity compared to wild-type. A transgenic cell may be one stably transfected with a gene which when expressed influences the rate of phagocytic activity for apoptotic cells. For example, the mammalian cells may be transfected with h1ced-6 or h2ced-6 as described above, preferably using any of the vectors mentioned herein in the description or drawings.

In another embodiment in accordance with the invention the phagocytes may be transfected with a DNA encoding the cell surface antigen CD36. Expression of CD36 is required for phagocytosis of apoptotic cells by human

macrophages that use either a phosphatidylserine receptor or the vitronectin receptor. (Fadok V.A.et al, J. Immunol 1998 Dec 1.161(11):6250-7.)

Transfection may be carried out by any of the methods described herein and preferably using a vector comprising a DNA sequence encoding CD36 as shown in Figure 31 or the entire vector of Figure 31.

The methods of the invention are all performed in a

multi-well plate format and are therefore particularly suitable for mid-to-high throughput screening. In a preferred embodiment, the multi-well plates have 96 wells, but the invention is also applicable to multi-well plates with another number of wells, which include but is not restricted to plates with 6, 12, 24, 384, 864, 1536 wells.

All of the methods of the invention require the detection of a signal which quantitates the phagocytosis of apoptotic cells in the presence of the 20 compound under test. It is an essential feature of the methods of this invention that this signal (also referred to as the read-out) is detected using a nonvisual detection means. As used herein the term 'non-25 visual detection means' refers to any means of detecting a signal which does not require visual inspection of the human eye including inspection through a microscope. The use of a non-visual detection system represents a major advantage over 30 previously known screening methods which require visual inspection of the cells by eye in order to detect uptake of apoptotic cells by phagocytes.

To allow for the non-visual detection of the apoptotic cells, in the high to mid-throughput screening in the phagocytosis assay, the reporter gene must be capable of generating a signal which is detectable by an

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automatic plate reader, such as the victor2 (Wallac, Turku, Finland). An automatic plate reader which detects a fluorescent signal is most preferred.

By generating a signal which can be read by an automatic multiwell plate reader quantitatve measurements can be made and this allows for the assessment of the effect of many compounds at once, as well as comparison of the effects between the compounds.

It is further pointed out that the compounds to be tested may be any of the types of compounds described above and that where a particular compound results in a reduced signal or no signal for the phagocytes, the phagocytes will be tested for viability to rule out non-specific toxicity of the compound in question.

In the non-limiting examples which follow reference is made to the following Figures:

FIGURE 1 shows the construction of 2416bp consensus sequence which was obtained from EST, RACE and colony hybridization (see Example 1). The sequence was compiled by using a a159394 as template and primers as indicated in multiple alignment. rcc stands for reverse complement. Both ced-6 and hced-6 are indicated above the multiple alignment; pGA101 was picked up by colony hybridization;

FIGURE 2 shows the consensus DNA sequence of h1ced-6 (2416 bp). Start and stop codons are in bold and underlined. Alternatively, spliced region is underlined;

FIGURE 3 shows the alternatively spliced DNA sequence of h2ced-6. Start and stop condon in bold and

underlined;

FIGURE 4 shows the amino acid sequence of hCED-6. Number of residues: 304, Molecular weight 34.4kDa. again the alternatively spliced region is underlined;

FIGURE 5 shows the amino acid sequence of h2CED-6, the alternatively spliced version;

- FIGURE 6 shows gel analysis of the nested PCR products generated as described in Example 3; the lanes are loaded as follows: (1) 100bp marker, (2) primary living neutrophils, (3) primary apoptotic neutrophils, (4) primary macrophages, (5) primary macrophages interacted with apoptotic neutrophils, (6) J774, (7) COS-1, (8) THP-1;
 - FIGURE 7 shows the DNA sequence of the commercially available Clonetech vector pEGFP-N3 comprising the Teporter gene GFP as used in Examples 4 and 8;

FIGURE 8 shows a plasmid map of pEGFP-N3;

FIGURE 9 shows the DNA sequence of plasmid pGA3104, as used in Examples 4 and 8, which comprises hlced-6 in the multicloning site of pEGFP-N3;

FIGURE 10 shows a plasmid map of pGA3104;

- FIGURE 11 shows a DNA sequence of commercially available plasmid pcDNA3.1/His/LacZ used for stable transfection of Ba/F3 cells (see Example 4);
- FIGURE 12 shows fluoresence intensity as a function of transfected cell concentration when β -galactosidase is reacted with the fluorogenic substrate fluorescein dib-D-galactopyranoside (FDG);

FIGURE 13 shows the effect of (FDG) concentration on the read-out of the assay of Example 5;

FIGURE 14 shows the effect of incubation time on the read-out of the assay of Example 5;

FIGURE 15 shows the effect of serum concentration in medium of Ba/F3 cells on the assay of Example 5;

FIGURE 16 shows the location of the epitopes in h1CED-6 used for generating polyclonal antibodies;

FIGURE 17 shows the DNA sequence of the plasmid pGA1028 (pBAD/His A/-hced-6) used in Example 7;

FIGURE 18 shows a plasmid map of pGA 1028;

FIGURE 19 shows the DNA sequence of commercially available Promega plasmid pGL2 which is suitable for introduction of reporter gene luciferase into Ba/K3 cells;

FIGURES 20 to 25 show the results of the immunoblots carried out in Example 7. In all these figures the lanes are loaded as follows:

- Lane 1: Prestained SDS PAGE Standards Low Range (Bio Rad Hercules, CA, USA),
- Lane 2: pBAD/His A (Invitrogen, Leek, The Netherlands)
 - Lane 3: pGA1028 (pBAD/HisA/-h1CED-6)
- FIGURE 20 shows gel stained with antibodies to the epitope EP 990044 as identified in Example 7 and control antibodies Anti-Xpress Ab (Invitrogen, Leek,

The Netherlands) and Mouse 1g, horseradish peroxidaselinked whole antibody (from sheep) (ECL Western blotting detection reagents and analysis system, Amersham Pharmacia Biotech, UK, England);

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FIGURE 21 shows gel stained with antibodies to epitope 990044 and immune serum as described in Example 7;

FIGURE 22 shows gel stained with antibodies to epitope 990045 as identified in Example 7 and control antibodies as described for figure 20;

FIGURE 23 shows gel stained with antibodies to epitope 990045 and immune serum as described in Example 7;

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FIGURE 24 shows gel stained with antibodies to epitope 990046 and with control antibodies as described for Figure 20;

FIGURE 25 shows gel stained with antibodies to epitope 990046 and with immune serum as described in Example 7:

FIGURE 26 shows the DNA sequence of the commercially available Clonetech vector pEGFP-C2 comprising the reporter gene GFP as used in Example 8;

FIGURE 27 shows a plasmid map of pEGFP-C2;

FIGURE 28 shows the DNA sequence of plasmid pGA3103 as used in Example 8 which comprises hlced-6 in the multicloning site of pEGFP-C2;

FIGURE 29 shows a plasmid map of pGA3103;

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FIGURE 30 shows Western blot of cell lysates from COSl cells transfected with MOCK (negative control for transfection), pEGFP-N3, pGA3103 and pGA3104; control lysates for actual co-immunoprecipitation from Ba/F3 cells incubated with or without the first antibody; positive control lysates from EGF-stimulated A431 cell lysates for anti-phosphotyrosine antibody. Blot A was probed with a mouse monoclonal 1gG2 which detects tyrosine-phosphorylated proteins in cell lysates; blot B was probed with polyclonal antibody which reacts with green fluorescent protein; and blot C was probed with rabbit antiserum to h1CED-6. MW of h1CED-6 is 34435.39; Mw of GFP is 26886.32; and Mw of the fusion protein GFP-CED-6 or CED-6-GFP is 62385.95;

FIGURE 31 shows the DNA sequence of plasmid pGA1058

which comprises a DNA sequence encoding the cell
surface receptor CD36 inserted in the multicloning
site of pEGFP-N3;

FIGURE 32 shows a plasmid map of pGA1058;

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FIGURE 33 shows the percentage annexin and propidium iodide positive cells in a cell population of Ba/F3 cells as a function of time after withdrawal of IL-3;

FIGURE 34 shows the effect of temperature on FDG incubation, live and apoptotic Ba/F3 cells were added to macrophage cell-line J774. After the phagocytosis assay, FDG (10μM) was incubated for 1h at 4°C, 20°C and for 10 and 20 min at 37°C.

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EXAMPLE 1

Extensive searches (tblastn) with the ced-6 sequence (Figure 2 Consensus DNA Sequence of hced-6) against the public domain databases (EST, Genbank, EMBL, Swissprot and PIR) revealed statistically significant homologies to some ESTS at the carboxyterminal region

of the protein (AA443368, AA431995, R33389, R53881). One Est (T48513) showed homology to the carboxyterminal of the PTB domain and the beginning of the charged region. For 5' RACE analysis a Marathon-5 ready cDNA colorectal adenocarcinoma, library was used from Clontech. The position of the primers used for RACE and sequencing is indicated in Figure 1. By subsequent cloning and sequence analysis additional sequence information was obtained. Using this 10 additional sequence information and subsequent rounds of database searching (blastn) revealed additional EST, which enabled us to construct a consensus of approx. 2400 bp. This sequence was further extended and verified by colony hybridization and sequencing 15 additional RACE products.

EXAMPLE 2 RNA Blots:

A human multiple tissue Northern (MTN-1, Clontech) containing in each lane 2 mg of poly A + RNA from eight different human tissues (heart, brain, placenta, lung, liver, skeletal muscle, kidney, and pancreas) and a MTN-II human multiple tissue Northern, 25 containing in each lane 2 mg of poly A + RNA from spleen, thymus, prostate, testis, ovary, small intestine, colon and peripheral leukocyte, were hybridized according to the manufacturer's instructions and washed out in 0.1 x SSC, 0.2% SDS at 55°C. Also from Clontech, a poly A + RNA blot from human cancer cell lines (melanoma G361, lung carcinoma A549, colorectal adenocarcinoma SW480, Burkitt's lymphoma Raji, lymphoblastic Leukemia Molt-4, chronic myelogenous leukemia K562, Hela S3 and promyelocytic 35 leukemia HL60) was tested.

Expression pattern of hCED-6 in normal human tissues.

and cancer cell lines by Northern blotting is shown in Table I below:

A) Human Multiple Tissue Northern (MTN) Blot B) Human Multiple Tissue Northern (MTN) Blot II C) Human Cancer Cell Line Multiple Tissue Northern (MTN $^{\text{TM}}$) Blot.

TABLE I

A)

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·	heart	brain	placenta	lung	liver	skeletal muscle	kidney	pancreas
Expression level	+		+++	+.		++	+	+
length (kb)	3,6		3.6	3,6		3.9	3,6	3.6

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B)

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	spleen	thymus	prostate	testis	ovary	small intestine	coton (mucosal lining)	peripheral blood leukocyte
Expression level	+		+	++	+	+	+	
length (kb)	3.6		3,6	3,9	3,6	3,6	3,6	

C)

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	promyelocytic leukemia HL-60	HeLa cell S3	chronic myetogenous leukemia K-562	lymphoblastic leukemia MOLT-4	Burkitt's∉lymphoma Raji	colorectal adeno- carcinoma SW480	lung carcinoma A549	melanoma G361
Expression level		++	+++			+++	+++	+
length (kb)		3.6	3.6			3.6	3 6	3.6

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EXAMPLE 3

Detection of the CED-6 (h1CED-6) and its splice variant (h2CED-6) in phagocytic cell lines.

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Cell line THP-1 (ATCC no: TIB-202), a human monocyte celline that can be differentiated into a macrophage cell with PMA (Sigma-Aldrich, St-Louis, MO, USA), was cultivated under standard conditions in RPMI 160 medium containing 2mM L-glutamine, 1.5g/L sodium bicarbonate, 4.5 g/L glucose, 10mM HEPES, 1 mM Sodium pyruvate, 0.05mM β-mercaptoethanol. (all purchased from gibcoBRL, Life Technologies, Merelbeke, Belgium)

- RNA has been isolated from this cell line using the RNeasy mini kit from qiagen (Westburg, Leusden, the Netherlands), according the instructions of the manufacture, or with minor modifications thereof.
- Starting from this RNA, first strand cDNA was generated using the Ready-To-Go T-primed First-strand kit from Pharmacia Biotech (Piscataway, NJ, USA), according the instructions of the manufacture, or with minor modifications thereof.

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The generated cDNA was used in a PCR protocol to generate DNA fragments using primers: oGA131: 5'-CGCAAGGATCCCCATGAACCGTGCTTTTAGCAGGAAG-3' 445-10934-13R: 5'-GATCTACTAGGTACTGGAG-3'

PCR was performed with the TaKaRa ex Taq kit (Takara Shuzo CO., LTD, Shiga, Japan) according the instructions of the manufacture, or with minor modifications, Plasmid pGA1025, harboring the hlced-6 gene was used as positive control.

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In summary:

PCR on the first-strand cDNA isolated from the Ready-To-Go T-primed First-strand kit contained the entire cDNA as made, 0.4 μ l oGA131 (100pmol/ μ l), 0.4 μ l 445-10934-13R (100pmol/ μ l), 0.5 μ l exTaq 5U/ μ l, 65.7 μ l water.

PCR on the positive control contained, 10 μ l buffer exTaq 10x, 10 μ l dNTP mix exTaq 10x, 0.4 μ l oGA131 (100pmol/ μ l), 0.4 μ l 445-10934-13R (100pmol/ μ l), 2 μ l pGA1025, 76.2 μ l water.

PCR-program:

 $2~\mu l$ of each PCR reaction and $1~\mu l$ from the positive control PCR reaction was used to perform a nested PCR, with following primers:

oGA131: see above

oGA141:5'-GCGGATGGTACCGTCGACTGCTGATACTTGAGTTATT CTCAG-3'

PCR was performed with the TaKaRa ex Taq kit (Takara Shuzo CO., LTD, Shiga, Japan) according the instructions of the manufacture, or with minor modifications.

The mastermix: 5 μ l buffer exTaq 10x, 5 μ l dNTP mix exTaq 10x, 0.2 μ l oGA131 (100pmol/ μ l), 0.2 μ l oGA141 (100pmol/ μ l), 0.5 μ l exTaq 5U/ μ l, 37.1 μ l water.

Program: 94°C 4'

10 μ l nested-PCR product was analyzed on gel using standard protocols (Molecular Cloning, a laboratory manual, Sambrook et al, 1989, CSHL press).

The above procedure was repeated for primary living neutrophils, primary apoptotic neutrophils, primary macrophages, primary macrophages interacted with apoptotic neutrophils, mouse monocyte cell-line J774 and COS-1 cells. The results are shown in Figure 6.

Remarkably, only in cell-line THP-1 could h1ced-6 and its splice variant h2ced-6 be detected (see lane 8 of Figure 6).

EXAMPLE 4

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Stable cell lines of human CED-6

99R, Interpulse delay= 0

J774 murine monocyte tumour cell line (Morland and Kaplan, 1978, Exp. Cell Res. 115:53-61; Morland and Kaplan, 1978, Exp. Cell Res. 115:63-72 Accession No ATCC TIB67 - also described as J774A.1) cultivated in DMEM, with glutamaxI, 10% myoclone serum (all from GIBCOBRL, Life Technologies, Merelbeke, Belgium), were transfected by electroporation, with the plasmids pEGFP-n3 (Clonetech, Palo Alto, CA, USA) (Figures 7 and 8), mock transfection, pGA3104, h1CED-6/GFP fusion (Figures 9 and 10) Salmon Sperm DNA; negative control.

Electroporation was performed with Easyject Plus electroporator system from Equibio Ltd (Immunosource, Halle-Zoersel, Belgium), using following protocol: 3×10^6 cells were placed in $800\mu l$ cell culture medium, and 30 μg DNA was added

The settings of the Easyject Plus electroporator were: double pulse:

Voltage I = 750V, Capacitor I = 25 μF , Resistance I =

Voltage II 150 V, Capacitor II = 1500 μ F, Resistance II = 99R, Optipulse option 3200 μ l of electroporated cells per construct were seeded into a 175 cm² culture flask, and selected with G418 antibiotic (400 μ g/ml) (Duchefa, Haarlem, The Netherlands) after 72h. Subclones of clones were obtained and checked for GFP expression.

EXAMPLE 5

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Phagocytosis assay

Preparing the phagocytes

Monocyte cell line J774 stably transfected with pEGFPn3 or pGA3104, or pGA1058 were plated at a density of 1 x 10⁵ in a black 96-well plate for 36h at 37 °C and 5% CO₂ in advance of performing the phagocytosis assay.

Preparing the apoptotic cells

- Growth factor dependent cell line Ba/F3 stably transfected with β-galactosidase as reporter gene is used as source of apoptotic cells. A suitable plasmid for transfecting Ba/F3 is pcDNA3.1/His/LacZ as shown in Figure 11. Ba/F3 cells which are IL-3 dependent mouse clones (Palacios and Steinmetz, 1985, Cell 41:727-734; Palacios et al, 1984, Nature 309:126-131), were grown in DMEM with glutamaxI, 10% FCS, 1% antibiotics (all from GIBCOBRL, ibid.), and 10% supernatant from WEHI-3 culture.

 30 WEHI-3 (ATCC no.: TIB-68) produces IL-3 when grown in
- WEHI-3 (ATCC no.: TIB-68) produces IL-3 when grown in culture medium: RPMI 1640 with glutamaxI, 10% FCS, 3.6μl β-mercaptoethanol per 1 litre. Ba/F3 cells were split ½ two days before the interaction assay (exponential growth phase) and Ba/F3 cells (5 x 106/ml) were cultured without growth factor IL-3 for 20h in advance of performing the assay. Apoptotic Ba/F3 cells were monitored by the

annexin/propidium iodide labeling Kit from Boeringher-Mannheim (Brussels, Belgium). Ba/F3 cells are early apoptotic if 20% annexin positive and less than 5% propidium iodide negative. Ba/F3 cells cultured with growth factor IL-3 were used as a negative control. Results of the annexin/propidium iodide test are shown in Figure 33.

Adding the apoptotic cells to the phagocytes

- 10 μ l Ba/F3 cells (1 x 10 7 cells/ml) were added to wells containing stably transfected J774 and to the negative control wells and incubated at 37 $^\circ$ C for periods ranging from 20 minutes to 5 hours after which the apoptoptic cells were removed from all wells.
- Phagocytes were washed three times in PBS buffer (GIBCOBRL, ibid.), being careful not to dislodge any of the cells.

Read-out

- Phagocytosis by the J774 cells of the apoptotic bodies was measured by detecting the β-galactosidase as expressed in the Ba/F3 cells. Detection was performed with a fluorogenic substrate, Fluorescein di-b-D-galactopyranoside (FDG) (Molecular probes, Eugene, OR,
- USA). 10 μ M FDG was added to the wells and incubated for 1h at room temperature in the dark. FDG is sequentially hydrolysed to FMG and fluorescein by the activity of the β -galactosidase, and the green fluorescein emission was measured in a standard plate reader using 480mm excitation, 520mm emission and the appropriate sensitivity settings.
 - For calibration purposes fluorescent read-out was determined for different Ba/F3 concentrations. The fluorescent read-out as a function of cell
- concentration is shown in Figure 12.

 Further experiments were carried out varying the concentration of FDG, the incubation time of the

assay, the temperature of the assay and the concentration of serum in the Ba/F3 medium. The results are shown in Figures 13, 14, 15 and 34 respectively.

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Compound Screening

The above described phagocytosis assay is used to screen compounds for their ability to influence the level of phagocytosis of apoptotic cells by professional phagocytes. The test compound or compounds can be added to the test wells approximately 30 minutes before addition of the Ba/F3 cells to the wells. Because of the multiwell format of the assay and automatic readout of fluorescence using standard equipment the assay is ideally suited to high throughput compound screening.

It will be understood that where any compound the presence of which results in no fluorescence or 20 reduced fluorescence compared to phagocytic cells not exposed to the compound, the cells in that well will be tested for viability using commercially available reagents such as the Live/Dead Viability/Cytotoxicity 25 Kit from Molecular Probes (Eugene, USA). This kit provides a two-colour fluorescence cell viability assay that is based on the simultaneous determination of live and dead cells with two probes, calcein AM and ethidium homodimer, that measure two recognised parameters of cell viability, intracellular esterase activity and plasma membrane integrity, respectively. This kit is suitable for use with fluoresence multiwell plate scanners. The presence of viable cells will confirm that the lack of fluorescence is due to the effect of the compound on phagocytic activity and 35 not just non-specific toxicity.

Furthermore any compound identified as an inhibitor or an enhancer of phagocytosis of apoptotic cells by the assay described above will be further tested to confirm the effect is medicated through CED-6. In the case of a compound identified as an enhancer of phagocytosis of apoptotic cells this can be achieved by carrying out a phagocytosis assay exactly as described above with J774 cells which are not transfected with hlced-6 or h2ced-6. If the compound is able to induce a phenotype in the J774 cells which is similar to the phenotype of those cells when transfected with hced-6 then it is an indication that the compound in question exerts its effect via CED-6 or via the CED-6 signal transduction pathway.

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Similarly, if a compound identified in the above-described assay is an inhibitor of phagocytosis of apoptotic cells it can be confirmed whether its effect is via CED-6 or the CED-6 signal transduction pathway by examining the phenotype of the transfected J774 cells exposed to the compound. Reversion to a wild-type phenotype is an indication of action via CED-6 signal transduction pathway.

25 <u>EXAMPLE 6</u>

Polyclonal antibodies directed to human CED-6
Polyclonal antibodies where raised in rabbits against the following ced-6 epitopes:
EP990044 H2N - NRA FSR KKD KTC CONH2

- EP990045 H2N CFL GST EVE QPK GTE CONH2
 EP990046 H2N CTR NGT QPP PVP SRS T CONH2
 Location of these epitopes in the ced-6 protein is shown in Figure 16.
- The polyclonals were raised by Eurogentec Bel, Herstal, Belgium, using following protocol:

 Day 0: taking of pre-immune serum followed by the

first immunisation

Day 14: second immunisation

Day 28: third immunisation

Day 38 : blood sampling (shipping 2ml)

5 Day 56: fourth immunisation

Day 66: blood sampling (shipping 2ml + 20ml)

Day 80 : complete bleeding.

EXAMPLE 7

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Testing Antibodies by Western Blot

Transformation of plasmid pGA1028(pBAD/His A-hCED-6) (see Figures 17 and 18) was done in TOP 10 competent cells. Furthermore pBAD/His was transformed in the same E. coli cells as a negative control. pBAS/HisA and E. coli TOP 10 were purchased from Invitrogen (Leek, The Netherlands).

The pBAD-vectors expression system was used, as it is known to be an efficient expression system. In the presence of arabinose, expression from pBAD is turned on while the absence of arabinose produces very low levels of transcription from pBAD. A pilot expression was carried out according the instructions of the manufacturer, in which the amount of arabinose was varied to determine the approximate amount of arabinose needed for maximum expression of your protein. The protocol according to the manufacturer (invitrogen, Leek, The Netherlands) was used.

30 Expression was scaled up using the same protocol.

Purification of protein was performed from the E. colicells transformed with pGA1028: 5 ml lysis buffer (10 ml TE 1x pH 8, 0.5 mg/ml lysozyme, 0.1mg/ml DNAse, 100 μ 1 1M CaCl₂ 400 μ 1 protease inhibitor 25x) was added to the pellet of a 50ml expression induced culture, and the pellet was resuspended in this lysis buffer.

The suspension was placed for 30 mins on ice and sonicated 3 times for 5" (high density), after which the suspension was treated with 3 cycles of freezedefreeze (liquid nitrogen - 42°C), and placed for 30 min at 37°C. The suspension was centrifuged for 5' at maximal speed. The pellet which contains the insoluble fraction and also the hCED-6 fusion protein was resuspended in 1 ml 2M urea and shaken for 5' at 1200 rpm. This suspension was centrifuged for 5' at maximal speed, and the supernatant was used for gel electrophoresis and Western blotting. $25 \mu 1$ supertant and $25 \mu 1$ premixed Laemmli Sample Buffer (Bio Rad-Hercules, CA, USA) was mixed.

Proteins from the negative control were not purified.

E. coli transformed with pBAD/His were prepared by pelleting 1 ml of induced E. coli culture, and resuspending the pellet in 1 ml of premixed Laemmli Sample Buffer (Bio Rad- Hercules, CA, USA). As such this suspension can be used for PAGE Gel electrophoresis.

Preparation of samples to load on a gel:
Both the samples were boiled for 5' and placed on ice
prior to loading. 25 µl samples were loaded on a
Ready Gel, 50 µl well TrisHCl, 4-15% (Bio RadHercules, CA, USA) and electrophoresis was performed
according to the manufacturer's instructions. The
proteins of the gel were transferred on nitrocellulose
membrane (Trans-blot Transfer medium, Bio RadHercules, CA, USA) with a MiniTransBlot
electrophoresis cell (Bio Rad- Hercules, CA, USA)
according to the instructions of the manufacturer (Bio
Rad- Hercules, CA, USA).

Western Blot was performed according to the providers of the antibodies and the detection kit.

A first antibody, in the western blots, immune serum or pre-immune serum of the rabbits was used in a dilution of 1/2000 in PBST (1.44 g/L KH2PO4, 90 g/L NaCl, 7.75 g/L Na2HPO4.7H20, 0.1% Tween)

- A second antibody: anti-rabbit, horseradish peroxidase-linked whole antibody (from donkey) diluted 1/4000 in PBST (0.1%) (ECL Western blotting detection reagents and analysis system, amersham pharmacia biotech, UK, England).
- All incubations were performed according to the manufacturer, with the following modifications. The first antibody was incubated overnight in PBST, instead of TBST. Detection of the antibodies was done according to the manufacturer's instructions (ECL
- Western blotting detection reagents and analysis system, Amersham Pharmacia Biotech, UK, England). Stripping and reprobing membranes after ECL detection kit, was done according to the manufacturer's instructions (ECL Western blotting detection reagents and analysis system, Amersham Pharmacia Biotech, UK, England).

Western Blot with control antibodies was done according the manufacturer's instructions of the antiHisA antibodies (invitrogen, Leek, The Netherlands),
The antibody, designated Anti-Xpress antibody diluted 1/5000 in PBST (0.1%) (invitrogen, Leek, The Netherlands) was used as first antibody.

Second antibody: Mouse Ig, horseradish peroxidaselinked whole antibody (from sheep) diluted 1/4000 in

and analysis system, Amersham Pharmacia Biotech, UK, England).

The staining of the antibodies in both experiments were performed according to the instructions of the

PBST (0.1%) (ECL Western blotting detection reagents

were performed according to the instructions of the manufacturer (ECL Western blotting detection reagents and analysis system, Amersham Pharmacia Biotech, UK,

England).

The results are shown in Figures 20 to 25.

5 EXAMPLE 8

<u>Interaction of H-CED-6 With Phospharylated Tyrosine</u>
Proteins

<u>Co-immunoprecipitation</u>

The antibodies raised against the three epitopes of h1CED-6 were used in western blotting to detect CED-6 interactions with phosphorylated tyrosine proteins and to identify CED-6 interacting proteins.

Transfection

Transfection of COS-1 cells was performed with plasmids pGA3103 (see Figures 26 to 29) and pGA3104 (see Figures 7 to 10) in a 175 cm² flask (1 x 107 cells). As a negative control: MOCK and pEGFP-N3 were used. Full length human ced-6 (in frame with GFP, both N and C terminal fusions, internal control) were investigated. COS-1 cells were transfected with lipofectamine Plus reagent (GIBCO-BRL). The protocol from Life Technologies was followed and the volumes that were used are shown in Table 2.

MOCK transfected cells are a negative control for transfection. In place of adding DNA, the solvent of the DNA only is added to the cells. Solvent of DNA is TE buffer, pH=8: 1M Tris (ICN) Ph=8 and 0.5 M EDTA (Merck-Belgolabo) pH=8 in H20.

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TABLE 2

Lipofectamine transfection (Life Technologies) of COS-1 cells in a 175 cm² flask

Culture flask	Construct	Conc. DNA	DNA	DNA	Optimem	Plus reagent	Optimem	Lipo fecta mine	Optimem	Optimem
4		րգ/բլ	μg	μ1	μl	μΙ	μΙ	μl	μl	ml
175 cm ²	MOCK	•	•	12 (TE)	1125	60	1125	90	2250	15
175 cm ²	pEGFP-N3	1	12	12	1125	60	1125	90	2250	15
175 cm ²	PGA3103	1	12	12	1125	60	1125	90	2250	15
175 cm ²	PGA3104	1	12 .	12	1125	60	1125	90	2250	15

As a positive control for phosphorylation, the β -chain of the IL-3 receptor of Ba/F3 cells which is phosphorylated was used.

COS-1 cell lysates were prepared using DIGITONIN (as gently as possible, not to disturb the interaction) and phosphatase inhibitors added (protease inhibitors, preferably cocktailpils or pefablock) to the lysis buffer.

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- Low stringency DIGITONIN based buffer:
 Buffer with DIGITONIN in 10 ml bidi
 - 1 % digitonin (Serva 19551, MW 1229.3) SERVA 2% stock= 250 mg in 12.5 ml
 - 10 mM triethanolamine pH 7.8 (Sigma-Aldrich; Bornem, Belgium10X stock 100 mM= 185,7 mg in 10ml pH 7.8 (5ml in 50ml)
 - 0.15 M NaCl (MW 58.44) 87.66 mg per 10ml
 - 2 mM Na₃VO₄ (Sigma-Alrich, Bornem, Belgium) 3.687 mg per 10 ml
 - 2 mM EDTA (Titriplex III; MW 372.24)
 (Darmstadt, Germany)
 7.444 mg per 10 ml
- 200 U/ml aprotinin Trazilol (Sigma-Aldrich, Bornem, Belgium)
 1 mg = 11 TIU = 9900 KU
 200X stock: 10 mg in 2 ml PBS = 49500 KU (50μl in 10ml)
 - 1 mM Pefabloc (Merck , Darmstadt, Germany) 2.4 mg per 10 ml

Lysis of cells

- Transfected cells were washed 2 x in PBS Dulbecco's (GIBCOBRL) in falcon
- Cells were scraped and pellet resuspended in $300\mu 1$ lysis buffer.

- All manipulations were carried out at 4°C.
- The preparation was centrifuged at 4000 rpm and the supernatant transferred to a new tube.

Preclearance

- Protein G sepharose CL-4B beads (Amersham
 Pharmacia, Roosendaal, the Netherlands) were
 supplied freeze dried in the presence of additives.
 These additives were washed away at neutral pH and
 ethanol replaced with lysis buffer.
- 50% v/v Protein G sepharose suspension:

 1 ml 50/50 v/v Protein G sepharose was pipetted and centrifuged at high speed for 5 sec. It was then aspirated and resuspended in equal volume of lysis buffer. Washing was repeated three times.
- To 300 μ l of lysate was added 50 μ l of protein G sepharose CL-4B beads (Amersham Pharmacia, ibid.) and this was reacted for 1 hour.
 - It was then centrifuged 10 sec at 14 000 rpm and 4°C and the supernatant transferred to a new tube.

Co-immunoprecipitation

- COS-1 lysates: 5 μ l anti-green fluorescent protein (GFP) polyclonal antibody rabbit (Immunosource, Halle-Zoersel, Belgium) was added.
- Lyophilized form was dissolved in 100 μl distilled water then frozen at -20°C
- Ba/F3 lysate number 5: 5 μl of rat antibody to β-chain of IL-3 receptor (Van der Heyden J., Devos R., Plaetinck G., Fache I., Fiers W., Tavernier J. 1991. Characterization of the murine IL-5 receptor complex with the use of a panel of monoclonal antibodies. Relationship to the murine IL-3 receptor. J Immunol. 147:3413-3418) was added.

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- 42 -

- Ba/F3 lysate number 6: no antibody was added.
- Samples were incubated between 4 h and 24 h (overnight) at 4 °C, rotating
- 50 μ l protein A beads were added and incubated for 1 hour at 4°C.
- Samples were centrifuged for 3 min at 3000 rpm (4°C)
- Beads were resuspended in 800 μ l lysis buffer, inverted several times or rotated for a few minutes and centrifuged at 3000 rpm for 3 minutes (4°C). This was repeated three times and on the last occasion the wash buffer was removed with a capillary tip.
 - Beads were suspended in 20 μl SDS loading buffer (with -mercapto)
 - Lysate number 7= EGF-stimulated A431 Cell lysate (positive control for anti-phosphotyrosine)
 (Upstate Biotechnology, cat. No. 12-302)
 - 2.5 μ l of β -mercaptoethanol was added to 100 μ l of lysate and samples boiled.
 - Samples were centrifuged for 3 min at 3000 rpm (4 °C) and SN was loaded on SDS PAGE using prestained SDS-Page standards low range from BioRad (cat.no 161-0305)

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Western-blotting

- Cell lysates were transferred to nitrocellulose with:
- Transfer buffer= 48 mM Tris, 39 mM glycine, 20% methanol, pH 9.2 (5.82 g Tris, 2.93 g glycine in H_2O , 200 ml methanol, to 1 L H_2O
 - Blocking buffer: 1x PBS, 0.1% Tween, 5% milk powder, incubate blot overnight
- Gel was probed with anti-phosphotyrosine (cat. 05-321, Upstate Biotechnology): 1 μ g/ml for 3h and

washed twice with PBS, 0.1% Tween for 5 min

- Proteins were visualized using 1:4000 goat antimouse horseradish peroxidase (cat.no RPN 2108, Amersham pharmacia biotech) as second Ab for 1h at RT.
- Blots were washed twice with PBS, 0.1% Tween for 5 min, twice with blocking buffer for 5 min and twice with $\rm H_2O$ (5min)

10 ECL Western blotting analysis system

ECL Western blotting detection reagents from Amersham Pharmacia Biotech (cat.no RPN 2108) were used.

Stripping and reprobing blot after ECL detection kit

The membranes were stripped of bound antibodies and reprobed. Membranes were stored wet in saran wrap at 4°C after each immunodetection.

- The membrane was submerged in stripping buffer (100 mM β-mercaptoethanol, 2% SDS, 62.5 mM Tris-HCl pH 6.7) and incubated at 50 °C for 30 min with occasional agitation.
- The membrane was washed for 2 x 10 min in PBS, 0.1%

 Tween at room temperature using large volumes of wash buffer.
 - The membrane was blocked by immersing in blocking buffer for 1h at RT.
- Immunodetection was performed with anti-green 30 fluorescent GFP and repeated with anti-human CED-6

Results

Western blots of all cell lysates probed either with anti-phosphotyrosine, anti-green fluorescent protein (GFP) or with rabbit sera against CED-6 are shown in

Figure 30, blots (A), (B) and (C). One band between 49 and 74K stained with anti-phospotyrosine is present in the COS-1 cell lysates transfected with fusion proteins of GFP and CED-6 and is not present in the control COS-1 cell lysates. By probing the western blot with anti-GFP and anti-CED-6 the same band between 49 and 74K was stained.

Conclusion

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Fusion proteins CED-6-GFP and GFP-CED-6 are both tyrosine phosphorylated. Their molecular weight is 62385.95K which represents the band between 49 and 74K that is stained positive for anti-

phosphotyrosine, anti-green fluorescent protein (GFP) and anti-CED-6.

EXAMPLE 9

Stable cell lines transfected with human cell surface receptor CD36.

J774 murine monocyte tumour cell line was transfected by electroporation with plasmid pGA1058 shown in Figure 31 and 32. The methods used were as described in example 4 for human ced-6.

The transfected cell-line was used as a positive control in carrying out phagocytosis assays using the protocol of Example 5.

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EXAMPLE 10

Generation of apoptotic particles starting from PC12.

The PC-12 cell-line(ATCC number: CRL-1721) (Mesner P.W., Winters T.R., Green S.H., (1992) J. Cell Biol.119:1669-1680, tends to grow in small clusters.

By addition of nerve growth factor-beta (50ng/ml final conc., Sigma), PC-12 cells differentiate into neuronal cells. By withdrawal of nerve growth factor after 5 days of treatment, programmed cell death in neuronal rat PC12 cells is induced.

The cells are cultured in RPMI 1640 (Life Technologies) with 2mM L-glutamine adjusted to contain 1.5g/L sodium bicarbonate, 4.5g/L glucose, 10mM HEPES and 1mM sodium pyruvate, 10% horse serum, 5% fetal bovine serum.

These cells can be tested for apoptotic character using the annexin/PI kit described above.

SEQUENCE LISTING

The nucleotide and amino acid sequences shown in the Figures herein are designated the following SEQ ID

5	-	Nos.

	•	
	SEQ ID NO: 1	Figure 1
	SEQ ID NO: 2	Figure 2
	SEQ ID NO: 3	Figure 3
10	SEQ ID NO: 4	Figure 4
	SEQ ID NO: 5	Figure 5
	SEQ ID NO: 6	Figure 7
	SEQ ID NO: 7	Figure 9
	SEQ ID NO: 8	Figure 11
15	SEQ ID NO: 9	Figure 17
•	SEQ ID NO: 10	Figure 19
·	SEQ ID NO: 11	Figure 26
	SEQ ID NO: 12	Figure 28
:	SEQ ID NO: 13	Figure 31
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CLAIMS:

1. An expression vector comprising a sequence of deoxynucleotides encoding a human CED-6 protein comprising the amino acid sequence of Figure 4 or Figure 5 or an amino acid sequence which differs from the amino acid sequence of Figure 4 or Figure 5 only in amino acid changes which are conservative of function.

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2. An expression vector as claimed in claim 1 comprising the sequence of deoxynucleotides shown from the transcription start codon to the transcription stop codon in Figure 2 or Figure 3.

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3. An expression vector as claimed in claim 1 or claim 2 which comprises a sequence of deoxynucleotides encoding a reporter gene positioned in said vector such that expression of said human CED-6 protein or functionally conserved variant thereof results in expression of a reporter protein from said reporter gene.

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4. An expression vector as claimed in claim 3 wherein said reporter gene is positioned 5' to the sequence of deoxynucleotides encoding said human CED-6 protein or functionally conserved variant thereof.

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5. An expression vector as claimed in claim 3 wherein said reporter gene is positioned 3' to the sequence of deoxynucleotides encoding said human CED-6 protein or a functionally conserved variant thereof.

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6. An expression vector as claimed in any of claims 3 to 5 wherein said reporter gene encodes green flourescent protein (GFP).

- 7. An expression vector as claimed in claim 4 which is pEGFP-C2 with a sequence of deoxynucleotides encoding a human CED-6 protein which comprises the sequence of amino acids as shown in Figure 4 or Figure 5 or a functionally conserved variant thereof inserted in the multicloning site.
- 8. An expression vector as claimed in claim 5 which is pEGFP-N3 with a sequence of deoxynucleotides encoding a human CED-6 homologue which comprises the sequence of amino acids as shown in Figure 4 or Figure 5 or a functionally conserved variant thereof inserted in the multicloning site.
- 9. An expression vector as claimed in claim 4 or 7 wherein said vector comprises the nucleotide sequence of Figure 28 (pGA3103).
- 10. An expression vector as claimed in claim 5 or 8 wherein said vector comprises the nucleotide sequence of Figure 9(pGA3104).
- 11. An expression vector as claimed in claim 1 or claim 2 wherein the human CED-6 protein or functionally conserved variant thereof expressed from said vector includes an epitope tag at the amino and/or the carboxy terminus thereof.
- 12. An expression vector as claimed in claim 11 wherein said epitope tag is His A.
 - 13. An expression vector as claimed in claim 11 which is pBAD/HisA with a sequence of deoxynucleotides encoding a human CED-6 protein comprising the sequence of amino acids as shown in Figure 4 or Figure 5, or a functionally conserved variant thereof, inserted therein.

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- 14. An expression vector as claimed in claim 12 which has the sequence of deoxynucleotides shown in Figure 17 (pGA 1028).
- 15. A mammalian cell-line transfected with an expression vector as claimed in any one of claims 1 to 13.
- 16. A mammalian cell-line as claimed in claim
 10 15 wherein said cell is selected from a fibroblast
 cell-line or an epithelial cell line.
- 17. A mammalian cell-line as claimed in claim 16 wherein said cell-line is selected from COS1, BHK21, L929, CV1, SWISS 3T3, HT144, IMR32, HEPG2, MDCK, MCF7, 293, Hela, A549, SW48 or G361.
 - 18. A mammalian cell-line as claimed in claim 15 wherein said cell-line is a primary cell-line.
 - 19. A mammalian cell-line as claimed in claim 18 wherein said cell-line is selected from human dermal FIBs, dermal keratinocytes, leucocytes, monocytes, lymphocytes, dendritic cells or macrophages.
 - 20. A mammalian cell-line as claimed in claim 19 which is mouse macrophage cell-line J774 or human monocyte cell-line THP-1.
- 21. A method for determining whether a compound is an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells which method comprises exposing transfected mammalian cells as claimed in any one of claims 15 to 20 to apoptotic particles and measuring the rate of phagocytic uptake of said particles by

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said transfected cells in the presence and absence of said compound.

- 22. A method as claimed in claim 21 wherein said transfected cells are exposed to said compound prior to addition of said apoptotic particles.
- 23. A method as claimed in claim 21 or 22 wherein said apoptotic particles are selected from the group consisting of apoptotic neutrophils, apoptotic lymphocytes and apoptotic erythrocytes which optionally have been opsonised.
- 24. A method as claimed in any of claims 21 to 23 wherein said apoptotic particles comprise adherent cell-line PC12.
- 25. A method as claimed in any of claims 21 to 23 wherein said apoptotic particles comprise the growth factor dependent mouse cell-line Ba/F3.
 - 26. A method as claimed in claim 25 wherein said Ba/F3 cells are rendered apoptotic by culturing in the absence of growth factor IL-3.
 - 27. A method as claimed in any one of claims 23 to 26 wherein the cells comprising said apoptotic particles are stably transfected with a reporter gene.
 - 28. A method as claimed in claim 27 wherein said reporter gene is selected from a gene encoding β -galactosidase, a gene encoding a fluorescent protein or a gene encoding a protein capable of generating luminesence.
 - 29. A method as claimed in claim 28 wherein

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said protein capable of generating luminescence is luciferase.

- 30. A method as claimed in claim 28 wherein said fluorescent protein is green fluorescent protein.
- 31. A method as claimed in claim 26 wherein said apoptotic particles comprises Ba/F3 cells stably transfected with β -galactosidase or luciferase.
 - 32. A method as claimed in claim 31 wherein the level of phagocytosis is detected by adding a substrate which is converted by said β -galactosidase to a fluorescent compound.
 - 33. A method as claimed in any one of claims 21 to 32 wherein if no phagocytosis or a reduced amount of phagocytosis is observed on exposure to the test compound, said mammalian transfected cells are examined for viability.
- 34. A method as claimed in claim 33 wherein if viable the phenotype of said mammalian transfected cells is compared with the phenotype of untransfected mammalian cells of the same cell-line.
- 35. A method as claimed in any of claims 21 to 32 wherein if an increased amount of phagocytosis is observed in the presence of the test compound, the method comprises the further steps of exposing said compound to an untransfected mammalian cell of the same cell-line and observing whether the compound induces a phenotype which is substantially the same as the phenotype exhibited by said transfected mammalian cell.

A compound identified by the method of any of claims 21 to 35 as an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells.

A method for determining whether a compound is an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cell which method comprises the steps of:

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micro-injecting into a mammalian cell a (1) human CED-6 protein comprising the sequence of amino acids shown in Figure 4 or Figure 5 or a sequence of amino acids differing from that shown in Figure 4 or Figure 5 only in amino acid changes conservative of function.

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exposing the mammalian cell produced in (2) step (1) to apoptotic particles and measuring the rate of phagocytic uptake of said particles by said cell in the presence and absence of said compound.

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A method as claimed in claim 37 wherein 38. said micro-injected mammalian cells are exposed to said compound prior to addition of said apoptotic particles.

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39. A method as claimed in claim 38 wherein said apoptotic particles are selected from apoptotic neutrophils, apoptotic lymphocytes and apoptotic erythrocytes which optionally have been opsonized.

35 A method as claimed in any of claims 37 or 40. 38 wherein said apoptotic particles comprise adherent cell-line PC12.

- 41. A method as claimed in any of claims 37 to 39 wherein said apoptotic particles comprise the growth factor dependent mouse cell-line Ba/F3.
- 42. A method as claimed in claim 41 wherein said Ba/F3 cells are rendered apoptotic by culturing in the absence of growth factor IL-3.
- 43. A method as claimed in any one of claims 39 to 42 wherein the cells comprising said apoptotic particles are stably transfected with a reporter gene.
- 44. A method as claimed in claim 27 wherein said reporter gene is selected from a gene encoding β-galactosidase, a gene encoding a fluorescent protein and a gene encoding a protein capable of generating luminescence.
- 45. A method as claimed in claim 44 wherein said protein capable of generating luminescence is luciferase.
- 46. A method as claimed in claim 44 wherein said fluorescent protein is green fluorescent protein.
- 47. A method as claimed in claim 42 wherein said apoptotic particles comprise Ba/F3 cells stably transfected with β -galactosidase.
 - 48. A method as claimed in claim 47 wherein the level of phagocytosis is detected by adding a substrate which is converted by said β -galactosidase to a fluorescent compound.
 - 49. A method as claimed in any of claims 37 to

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48 wherein the mammalian cell is a fibroblast cell or an epithelial cell.

- 50. A method as claimed in claim 49 wherein the mammalian cell is selected from COS1, BHK21, L929, CV1, SWISS 3T3, HT144, IMR32, HEPG2, MDCK, MCF7, 293, Hela, A549, SW48 or G361.
- 51. A method as claimed in any of claims 37 to 48 wherein said mammalian cell is a primary cell.
 - 52. A method as claimed in claim 51 wherein said mammalian cell is selected from human dermal FIBs, dermal keratinocytes, leucocytes, monocytes or macrophages.
 - 53. A method as claimed in claim 52 wherein said mammalian cell is a mouse macrophage cell J774 or a human monocyte cell THP-1.
 - 54. A method as claimed in any one of claims 37 to 53 wherein if no phagocytosis or a reduced amount of phagocytosis is observed on exposure to the test compound, said mammalian transfected cells are examined for viability.
 - 55. A method as claimed in claim 54 wherein, if viable, the phenotype of said mammalian transfected cells is compared with the phenotype of untransfected mammalian cells of the same cell-line.
 - 56. A method as claimed in any of claims 21 to 32 wherein if an increased amount of phagocytosis is observed in he presence of the test compound, the method comprises the further steps of exposing said compound to an untransfected mammalian cell of the same cell-line and observing whether the compound

induces a phenotype which is substantially the same as the phenotype exhibited by said transfected mammalian cell.

- 5 57. A compound identified by the method of any of claims 37 to 56 as an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells.
- 10 58. A method for determining whether a compound is an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells which method comprises the steps of:
- 15 (1) micro-injecting or transfecting into a mammalian cell a vector expressing RNA antisense to all or a portion of the sequence of nucleotides shown in Figure 2 or Figure 3;
 - (2) exposing the mammalian cell produced in step (1) to apoptotic particles and measuring the rate of phagocytic uptake of said particles by said cell in the presence or absence of said compound.
- 59. A method as claimed in claim 58 wherein said antisense RNA comprises a sequence of nucleotides which is capable of hybridizing to a sequence of nucleotides as shown in Figure 2 or Figure 3 under conditions of stringency which are higher than 2xSSC; 0.1% SDS; 25°C to 50°C.
- 60. A method as claimed in claim 58 or claim 59 comprising the features of any one of claims 38 to 56.

61. A compound identified by the method claims 58 to 60 as an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells.

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- 62. A peptide which comprises a fragment of a human CED-6 homologue having an amino sequence as shown in Figure 4 wherein said fragment includes the sequence of amino acids NRAFSRKKDKTC, FLGSTEVEQPKGTE or TRNGTQPPPVPSRST.
- 63. A peptide as claimed in claim 62 consisting of the sequence of amino acids NRAFSRKKDKTC, FLGSTEVEQPKGTE or TRNGTQPPPVPSRST.

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64. An antibody preparation comprising antibodies directed to one or more of the following epitopes of human CED-6 homologue as shown in Figure 4: NRAFSRKKDKTC, FLGSTEVEQPKGTE or TRNGTQPPPVPSRST

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65. An antibody preparation comprising antibodies directed to the human CED-6 homologue epitope NRAFSRKKDKTC.

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66. An antibody preparation comprising antibodies directed to the human CED-6 homologue epitope FLGSTEVEQPKGTE.

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- 67. An antibody preparation comprising antibodies directed to the human CED-6 homologue epitope TRNGTQPPPVPSRST.
- 68. An antibody preparation as claimed in any one of claims 63 to 66 wherein said antibodies are polyclonal antibodies.
 - 69. A method for diagnosing a disease

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associated with the over or under expression of human CED-6 protein in phagocytic cells in an individual which comprises:

- 5 (a) obtaining a sample of phagocytes from said individual;
 - (b) exposing said phagocytes to an antibody preparation as claimed in any of claims 64 to 68;
 - (c) quantitatively measuring the presence of any immune complexes formed between said antibodies and said CED-6 protein; and
 - (d) comparing the amount of immune complex formed with that formed using phagocytes from a control individual.
- 70. A method for determining whether a compound is an inhibitor or an enhancer of a signal transduction pathway which promotes phagocytosis of apoptotic cells which method comprises:
- 25 (a) exposing a mammalian cell transfected with an expression vector as claimed in any one of claims 1 to 14 to the compound to be tested;
- (b) exposing said mammalian cell to an antibody preparation as claimed in any of claims 64 to 68;
- (c) quantitatively measuring the presence of any immune complex formed between said antibodies and protein expressed by said cells; and

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- (d) comparing the level of immune complex detected with the amount of immune complex detected in a mammalian cell transfected as described in step (a) which has not been exposed to said compound.
- 71. A method as claimed in claim 70 wherein said mammalian cell is selected from COS1, BHK21, L929, CU1 SWISS 3T3, HT144, IMR32, HEPG2, MDCK, MCF7, 293, Hela, A549, SW48 or G361.
- 72. A method as claimed in claim 71 wherein said mammalian cell is a COS1 cell.
- 73. A method as claimed in claim 70 wherein the mammalian cell is a human dermal FIB, dermal keratinocyte, leucocyte, monocyte or macrophage.
- 74. A method as claimed in claim 73 wherein said cell is mouse monocyte cell J774 or human monocyte cell THP-1.
 - 75. A fusion protein which comprises:
- 25 (1) a sequence of amino acids as shown in Figure 4 or Figure 5 or a sequence of amino acids which differs from the sequence shown in Figure 4 or Figure 5 only in amino acid changes conservative of function; and
- (2) a protein which is the expression product of a reporter gene.
- 76. A fusion protein as claimed in claim 75 which is obtained by expression of the GFP and h1ced-6 encoding sequences shown in Figures 9 or 28.
 - 77. A fusion protein which comprises:

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- (1) a sequence of amino acids as shown in Figure 4 or Figure 5 or a sequence of amino acids which differs from the sequence shown in Figure 4 or Figure 5 only in amino acid changes conservative of function, and
- (2) an epitope tag.
- 78. A fusion protein as claimed in claim 77 which is obtainable by expression of the HisA and hlced-6 encoding sequences shown in Figure 17.
- 79. A method of identifying a compound which is an enhancer or an inhibitor of phagocytosis of apoptotic cells which comprises:
 - a) exposing a mammalian professional or semiprofessional phagocyte to an apoptotic
 mammalian cell which has been stably
 transfected with a reporter gene capable of
 generating a signal detectable without
 microscopy, in the presence and absence of
 the compound to be tested,
- 25 b) removing any apoptotic cells which are not engulfed by said phagocytes and
 - c) detecting any signal of the reporter gene from said phagocytes;

wherein any difference in signal in the presence of said compound compared to the signal in the absence of said compound is an indication that said compound is an inhibitor or an enhancer of phagocytosis of apoptotic cells.

80. A method as claimed in claim 79 wherein

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said phagocyte is mouse macrophage cell-line J774 or human monocyte cell-line THP-1.

- 81. A method as claimed in claim 80 wherein the monocyte cell-line is cultured under conditions to differentiate it into macrophages prior to exposure to said apoptotic particles.
- 82. A method as claimed in any of claims 79 to 81 wherein said phagocyte is a transgenic cell.
 - 83. A method as claimed in claim 82 wherein said phagocyte has been transfected with an expression vector as claimed in any of claims 1 to 14.
 - 84. A method as claimed in claim 82 wherein said phagocyte has been transfected with an expression vector encoding the cell surface receptor CD36.
 - 85. A method as claimed in claim 84 wherein said phagocyte has been transfected with a vector as shown in Figure 31.
 - 86. A method as claimed in any of claims 79 to 85 wherein said apoptotic cells comprise the adherent cell-line PC12.
- 30 87. A method as claimed in any one of claims 79 to 85 wherein said apoptotic cells comprise the growth factor dependent mouse cell-line Ba/F3.
- 88. A method as claimed in claim 26 wherein said Ba/F3 cells are rendered apoptotic by culturing in the absence of the growth factor IL-3.

89. A method as claimed in claim 88 wherein said cells are considered apoptotic if about 20% annexin positive and less than about 5% propidium iodide negative.

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- 90. A method as claimed in any of claims 79 to 89 wherein said reporter gene is selected from a gene encoding β -galactosidase, a gene encoding a fluorescent protein or a gene encoding a protein capable of generating luminescence.
- 91. A method as claimed in claim 90 wherein said protein capable of generating luminescence is luciferase.

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92. A method as claimed in claim 91 wherein said apoptotic cell has been stably transfected with a plasmid exhibiting the expression characteristics of PGL2control shown on Figure 19.

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93. A method as claimed in claim 92 wherein said apoptotic cell has been stably transfected with a plasmid comprising the sequence of deoxynucleotides shown in Figure 19.

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94. A method as claimed in any one of claims 79 to 89 wherein fluorescent protein is green fluorescent protein (GFP).

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95. A method as claimed in claim 94 wherein said apoptotic cell has been stably transfected with a plasmid exhibiting the expression characteristics or a plasmid as shown in Figure 10 or Figure 29.

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96. A method as claimed in claim 95 wherein said apoptotic cell has been transfected with a plasmid comprising the sequence of nucleotides shown

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in Figure 9 of Figure 28.

- 97. A method as claimed in any of claims 79 to 89 wherein said apoptotic cells have been stably transfected with a plasmid expressing b-galactosidase.
- 98. A method as claimed in claim 97 wherein said plasmid has the expression characteristics of the plasmid shown in Figure 11.
- 99. A method as claimed in claim 98 wherein said plasmid comprises the sequence of deoxynucleotides shown in Figure 11.
 - 100. A method as claimed in any of claims 79 to 89 wherein said apoptotic particles comprise cellline Ba/F3 stably transfected with β -galactosidase.
 - 101. A method as claimed in claim 100 wherein the level of phagocytosis is detected by adding a substrate which is converted by said b-galactosidase to a fluorescent compound.
 - 102. A method as claimed in any one of claims
 79 to 101 wherein if no phagocytosis or a reduced
 amount of phagocytosis is observed on exposure to the
 test compound, said phagocytes are tested for
 viability.
 - 103. A method as claimed in any of claims 79 to 102 wherein said phagocytes are cultured in multiwell plates the apoptotic cells and the test compounds being added to the individual wells thereof.
 - 104. A method as claimed in any preceding claim

wherein the signal from said reporter gene is detected by an automatic plate reader.

- 105. A method as claimed in claim 101 wherein the signal from the reporter gene is detected by an automatic plate reader capable of detecting a fluorescent signal.
- 106. A compound identified as an inhibitor or enhancer of phagocytosis of apoptotic cells by the method of any claims 79 to 105.
 - 107. A method as claimed in any of claims 22 to 35, 39 to 56, and 58 to 60 wherein phagocytic uptake is measured by non-microscopic means.
 - 108. A method as claimed in claim 107 wherein said non-microscopic means is a multi-well plate reader.

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109. A method as claimed in claim 108 wherein said multi-well plate reader measures luminescence. fluorescence or performs spectrophotometric detection.

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- 110. A method as claimed in any of claims 79 to 105 having the features of claims 108 and 109.
- 111. A method for diagnosing a disease

 30 associated with the over- or under-expression of human CED-6 in phagocytic cells in an individual, which method comprises:
 - (a) obtaining a sample of phagocytes from said individual,

- (b) isolating RNA from said phagocytes,
- (c) preparing cDNA from said RNA,
- (d) performing a first PCR reaction on said

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CDNA,

- (e) performing a second (nested) PCR on the reaction product of said first PCR reaction,
- (f) quantitatively and qualitatively measuring the presence of CED-6 RNA by analysing the reaction products from the first and second PCR,
- (g) comparing the amount and type of reaction products formed in the first and second PCR with that of the reaction products formed using phagocytes from control individuals.
- 112. A method as claimed in claim 111 wherein said PCR is performed with primers derived from the sequence of human CED-6, or derived from the vector used in the generation of cDNA.
- 113. A method as claimed in claim 111 or 112
 wherein said first PCR is performed with primers having nucleotide sequences:
 - 1) cgcaaggatccccatgaaccgtgcttttagcaggaag
 - 2) gatctactaggtactggag
- 114. A method as claimed in any of claims 111, 112 or 113 wherein said second PCR is performed with primers having nucleotide sequences:
 - 1) cgcaaggatccccatgaaccgtgcttttagcaggaag
 - 2) gcggatggtaccgtcgactgctgatacttgagttattctcag

	F/G. 1.		1/56		
	10.1.		,,00		
	1				50
consensus	GGTGATGAGC	ССТТСССТТС	TCGCTCCGAC	ТССТАВАТТС	•
Sea	GGTGATGAGC	CCTTGGGTTC		TGCTAAATTC	GCTTGGCCGG
thc117484	TGATGAGC	CCTTGGGTTC			GCTTGGCCGG
	IGATGAGC	CCIIGGIIC	ICGCICCGAC		
r65982					GCTTGGCCGG
aa159394	GGTGATGAGC	CCTTGGGTTC	TCGCTCCGAC	TGCTAAATTC	GCTTGGCCGG
aa369714	TGATGAGC	CCTTGGGTTC	TCGCTCCGAC	TGCTAAATTC	GCTTGGCCGG
•					
	51	-	•		100
consensus	GTCCACCTTC	TCGTGGCCTC	ACTCGCCACA	CGGATCAGAA	TCCGGAGCAG
Se q	GTCCACCTTC		ACTCGCCACA	•	
thc117484	GTCCACCTTC	TCGTGGCCTC			TCCGGAGCAG
r65982	GTCCACCTTC		ACTCGCCACA		TCCGGAGCAG
4.18.18					
aa159394	GTCCACCTTC	_ ,	ACTCGCCACA		TCCGGAGCAG
aa369714	GTCCACCTTC	TCGTGGCCTC	ACTCGCCACA	CGGATCAGAA	TCCGGAGCAG
	101				150
consensus	GCAGTTCTCT	CTATTCTGAG	GCTCCTGCGG	C TGCC GCG	CTGACTTCCC
Seq	GCAGTTCTCT	CTATTCTGAG	GCTCCTGCGG	C TGCC GCG	CTGACTTCCC
thc117484	GCAGTTCTCT	CTATTCTGAG	GCTCCTGCGG	C.TGCCGGC.	TGACTTCCC.
r65982	GCAGTTCTCT	CTATTCTGAG	GCTCCTGCGG		TGACTTCCC.
aa159394	GCAGTTCTCT	CTATTCTGAG	GCTCCTGCGG	CNTGCCNGCG	TGACTTCCCG
		CTATTCTGAG		_	
aa369714	GCAGTTCTNT	CIAIICIGAG	GCICCINCGG	C. IGCCGCGC	TGACTTCCC.
	151				. 200
consensus	TGTGTGGNGG	AGGGAACTCT	GGGCAGGCTG	GTTTTCTTGG	AATGTGTTTA
Seq	TGTGTGCGGG	AGGGAACTCT	GGGCAGGCTG	GTTTTCTTGG	AATGTGTTTA
thc117484	TGTGTGCGGG	AGGGAACTCT	GGGCAGGCTG	GTTTTCTTGG	AATGTGTTTA
r65982	TGTGTGCGGG	AGGGAACTCT	GGGCAGGCTG	GTTTTCTTGG	AATGTGTTTA
aa159394	TGTGTGGNGG	AGGGAACTCT	GGGCAGGCTG	GTTTTCTTGG	AATGTGTTTA
aa369714		•	GGGCAGGCTG		AATGTGTTTA
		7.0000101			
	201				250
			33 <i>0</i> 3 <i>0</i> 0 33		'
consensus	CGAI.GITGA	AIGGGACIIG	AACAGGAA		
	•		~ 3 - 6 .	primer oGA1	.03
	•	primer o			. •
Seq	CGAT GTTGA	ATGGGACTTG	AACAGG AA	GCTGGACGCT	GCA GCTGGA
r65983rcc		CTTG	AAACGGGNAA	CCGGGCCNCT.	GCAAGCNGGA
thc117484	CGAT.GTTGA	ATGGGACTTG	AACAGGAA	GCTGGACGCT	GCA.GCTGGA
r65982	CGAT.GTTGA	ATGGGACTTG	AACAGGAA	GCTGGACGCT	GCA.GCTGGA
aa159394	CGAT.GTTGA	ATGGGACTTG	AACAGGAA	GCTGGACGCT	GCA.GCTGGA
aa369714	CGATTGTTGA	ATGGGACTTG	AACAGGAA	GCTGGACGCT	GCA
				,	
	251				300
	• •	<i>C</i>	ጥ አ ጥር! አ ጥጥረ! ረ	እ <i>ጥርጥር</i> እጥአጥአ	•
consensus Seq	ACTAGCGTGC			ATCTGATATA	
	ACTAGCGTGC	C AAGTTATT	TATGATTCC		-
r65983rcc	ACTACCGTGC	CCAAGTTATT	TATGANCCCC	ACCTGATATA	•
thc117484	ACTAGCGTGC	C.AAGTTATT	TATGATTCC.	ATCTGATATA	CATAGGAGAG
r65982	ACTAGCGTGC	C.AAGTTATT	TATGATTCC.	ATCTGATATA	CATAGGAGAG
aa159394	ACTAGCGTGC	C. AAGTTATT	TATGATTCC.	ATCTGNTATA	CATAGGAGAG
	•			•	•
	301			•	350
consensus		GAAGAATTCT	GATGGCAACT	GTATGATAG	
, , , , , , , , , , , , , , , , , , ,	Tablet Cities	0.10.4.11.01		•	-10934-02F
			w i		10234-02F
	3330m 0505	033033mm	•	er oGA102	, , , , , , , , , , , , , , , , , , ,
Seq	AAACT GATA	GAAGAATTCT	GATGGCAACT	GTATGATAG	AAGCTAT AT
oGA102					TA
r65983rcc	AAACT.GATA	GAAGAATTCT	GATGGCAACT	.GTATGATAG	AAGCTAT.AT
thc117484	AAACT.GATA	GAAGAATTCT	GATGGCAACT	.GTATGATAG	AAGCTAT.AT
r65982	AAACT.GATA	GAAGAATTCT	GATGGCAACT	.GTATGATAG	AAGCTAT.AT
aa159394	AAACTTGATA	GAAGAATTCT	GATGGCAACT	.GTATGATAG	AAGCTAT.AT
	SUBS	TITUTE SHE	ET (RULE 26)	•
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		•		2/56		
	F/G	1. (CONTIL	VIIED)	-/ • •		
	, , , , ,					
		351				400
,	consensus	<u>AAAGTCAAGT</u>	GTCCATTTTC	TTTCAACTAT	ATTTGAGCAT	ACCCAGGATT
	Seq	AAAGTCAAGT	GTCCATTTTC	TTTCAACTAT	ATTTGAGCAT	ACCCAGGATT
	oGA102		GTCCATTTTC		ATTTGAGCAT	•
	r65983rcc	AAAGTCAAGT	GTCCATTTTC	TTTCAACTAT	ATTTGAGCAT	ACCCAGGATT
	thc117484	AAAGTCAAGT	GTCCATTTTC	TTTCAACTAT	ATTTGAGCAT	ACCCAGGGTT
	r65982	AAAGTCAAGT	GTCCATTTTC		ATTTGAGCAT	
	aa159394	AAAGTCAAGT	GTCCATTTTC		ATTTGAGCAT	
,						
hCED-6	•					M N R
		401				450
	consensus		AACTGAACAT	ттатттссст	GATCCTCATC	
		11110100100	7210107111111111	•	imer 445-10	
	Seq.	таастестес	ል አ <i>ር</i> ሞርአ አርአጥ		GATCCTCATC	
	oGA102		•	•	GATCCTCATC	
	r65983rcc					
	thc117484		•		GATCCTCATC	
			•		GATCCTCATC	· · · · - ·
	r65982		•		GATCCTCATC	
	aa159394	TAAGTCGTGG	AACTGAACAT	TAT		
GED 4						
CED-6	•	MAKDIYKTFK	RSVSGIVGGN	NINGEGSSSP	STSAPQVKYR	GGTG
					•	
CED-6	•		.***	R T W	I H P	P D Y L
hCED-6		A F S	R K K D	K T W	I H P M H T	P E A L
•		451			-	500
	consensus	GCTTTTAGCA	GGAAGAAAGA	CAAAACATGG	ATGCATACAC	CTGAAGCTTT
	Seg	GCTTTTAGCA	GGAAGAAAGA	CAAAACATGG	ATGCATACAC	CTGAAGCTTT
•	oGA102	GCTTTTAGCA	GGAAGAAAGA	CAAAACATGG	ATGCATACAC	CTGAAGCTTT
	r65983rcc	GCTTTTAGCA	GGAAGAAAGA	CAAAACATGG	ATGCATACAC	CTGAAGCTTT
•	thc117484	GCTTTTAGCA	GGAAGAAAGA	CAAAACATGG	GTGCTNACAC	CTGAAG.NTT
	r65982	GCTTTTAGCA	GGAAGAAAGA	CAAAACATGG	GTGCTNACAC	CTGAAG.NTT
			•	•		•
CED-6		I N G	H V E	Y V A R	F L G	C V E
hCED-6	·	S K H	FIP	Y N A K	F L G	S T E
-		501				5 50
	consensus	ATCAAAACAT	TTCATTCCCT	ATAATGCAAA	GTTTCTTGGC	AGTACAGAAG
,	Seq	ATCAAAACAT	TTCATTCCCT	ATAATGCAAA	GTTTCTTGGC	AGTACAGAAG
	oGA102	ATCAAAACAT	TTCATTCCCT	ATAATGCAAA	GTTTCTTGGC	AGTACAGAAG
	r65983rcc	ATCAAAACAT	TTCATTCCCT	ATAATGCAAA	GTTTCTTGGC	AGTACAGAAG
•	thc117484		TTCTTTCCNA			
• • •	r65982	ATCAAAAC.N	TTCTTTCCNA	TTT		
	•					
CED-6		T P K A	N G S	D V A	REAI	H A I
hCED-6		V E Q P	· ·	D V A E V V	R E A I R D A V	R K L
		551				600
	consensus		AAAAGGAACA	GAAGTTGTGA	GAGATGCTGT	
	Sea	· ·			GAGATGCTGT	•
	oGA102		•		GAGATGCTGT	
•	r65983rcc				GAGATGCTGT	
	-0000100	TOOMAGAGE	MUMBUURARA	OWWAITATOW	GROWING IGI	AAGGAAACIA
CED-6		מ מ	י ד ת פ	ם מ מ		T 0 55
hCED-6		R F Q	R D L K	R S E	QTRETAK	L Q K V
HCED - 0	· .	K F A	R H I K	K S E	G Q K	I P K V
	000000	601	0101m1mc11	0111mm	0000000	650
	consensus				GGCCAGAAAA	
	. Seq	•			GGCCAGAAAA	•
	oGA102				GGCCAGAAAA	
	r65983rcc	AAGTTTGCAA	GACATNTCAA	GAAATCTGAA	GGCCAAAAA	AAAAAAAG.

.AGTTTGCAA GACATATCAA GAAATCTGAA GGCCAGAAAA TTCCTAAAGT

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FIG. 1. (CONTINUED)

•	* ~	* * *	*	*	* *
CED-6	EIR	I S I	D N V I	I A D	I K T
hCED-6	E L O	I S I	Y G V K	I L E	РКТ
	651				700
CORCOROUG	GGAGTTGCAA	አ ጥአ ጥ <i>ር</i> ነ አ ጥጥጥ	ATGGAGTAAA	አአምሞሮሞአር:አአ	
consensus					·
Seq	GGAGTTGCAA			AATTCTAGAA	•
oGA102	GGAGTTGCAA		•	AATTCTAGAA	
r76378	GGAGTTGCAA	ATATCAATTT	ATGGAGTAAA	AATTCTAGAA	CCCAAAACAA
CED-6	K A P M	Y T F	P L G	R I S F	CAD
hCED-6	K E V Q	H N C	Q L H	R I S F	CAD
	701				750
consensus	AGGAAGTTCA	ACACAATTGC	CAGCTTCATA	GAATATCTTT	TTGTGCAGAT
Seq	AGG				
oGA102	AGG				
r76378		ACACAATTGC	CAGCTTCATA	GAATATCTTT	TTGTGCAGAT
d82787	AGOAAGIICA	CAATTGC		GNAATATCTTG(
462787		CAAIIGC	CAGCIICAIA	JNAATATCTTG	GGNGIGCAGAI
		n v n 11	B C T	* * * *	B C 3 C
CED-6	D K D	D K R M	FSF	IARA	EGAS
hCED-6	D K T	D K R I	FTF	I C K	D S E S
	751				800
consensus			ATTCACTTTC		
r76378		-	ATTCACTTTC		
d82787	GATAAAACTG	ACAAGAGGAT	ATTCACTTTC	ATATGCAAAG	ATTCTGAGTC
	•		•		
CED-6	G K P	S C Y	A F T S	E K L	A E D
hCED-6	N K H	L C Y	V F D S	E K C	A E E
	801				850
consensus	AAATAAACAT	TTGTGCTATG	TATTTGACAG	CGAAAAGTGT	GCTGAAGAGA
Seq					CTGAAGAGA
oGA102					. CTGAAGAGA
r76378	AAATAAACAT	TTGTGCTATG	TATTTGACAG		GTAAGTATCC
aa307982	MATRICAL	11010040			GCTGAAGAGA
•	· AAATAAACAT	TTGTGCTATG	TATTTGACAG		TGCTGAAGAGA
d82787	· AAAIAAACAI	TIGIGCIAIG	INTITOACAG	COMMANDIO	·
ann c	· .	T 0 E	· · · · · · · · · · · · · · · · · · ·	7 3 32	K R F
CED-6	ITLT	I G E	AFD	L A Y	
hCED-6	I T L T	I G Q	A F D	L A Y	
	851				900
consensus	TCACTTTAAC	AATTGGCCAA	GCATTTGA	CCTGGCATAC	<u>.</u>
pGA101	`				TC
Seq	•	AATTGGCCAA		·	AGGAAATTTC
oGA102	•		GCATTTGA	-	AGGAAATTTC
r76378	CAGATGTTGT	AGGGGTGGTT	TGTTCTGTTT	TATAAGNCC	GGGGATTGTC
aa307982	TCACTTTAAC	AATTGGCCAA	GCATTTGA	CCTGGCATAC	AGGAAATTTC
d82787	TCACTTTAAC	AATTGGCCAA	GCATTTGNN	CTGGCATAC	AGGAAATTTC
				•	
CED-6	L D K	N R T S	L E N	QK	Q I Y I
hCED-6	L D K L E S			R K	Q I A G
	901				950
consensus		GAGGAAAAGA	TGTTGAAA <u>CA</u>	AGAAAAC	AGATCGCAGG
, (Jone Cire de	_,,,_,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	and the second s			oGA107-F
•			Dria	ner 445-109	·-
·			E T T (-10934-08-R
-03101	מארטאא מיריאר	מאממא א א א מא	TGTTGAAACA	•	
pGA101				•	
Seq			TGTTGAAACA		
oGA102			TGTTGAAACA		
aa307982			TGTTGAAACA		
d82787	TNGAA.TCAG	GAGGAAAAGA	TGTTGAAACA	AGAAAAC	AGATCGCAGG
. 402707					

SUBSTITUTE SHEET (RULE 26)

	E/G. 1. [C	?01/ = /	<i>\\\\</i>	a)	4	1/5	6								
	10. 1. [6	DIVIII	VUE)												
CED-6 hCED-6			K K D K	K R	I I	V Q	Ð	L L	E T E T		E N	-	V E	L	I K
ncab-6		951	γ r.	K	1	¥	D	L	<u>.</u> .		<u> </u>	4 f ₇	E	_	1000
	consensus	GTTAC	AAAA	AGA	ATC	CAAG	ACT	CTAC	BAAAC	AG.	AAA	TAT	GGA	ACT	TAAA
	pGA101	GTTAC											_		TAAA
	Seq oGA107	GTTAC	AAAA	AGA	ATC	CAAG	AC'I	l'TAG	BAAAC	AG	AAAA	TAT	GGA	ACT	AAAT AAA
	OGA107	GTTAC	AAAA	AGA	ATC	CAAG	ACT	TAG	AAAC	AGG	AAA	TAT	GGA	ACT	
	r76378	CTTG.						· · · •							
	aa307982	GTTAC													
	d82787	GTTAC	AAAAA	AGA	CTC	CANG	ACI	TAC	AAAC	AG .	M MM	TAT	GGT	• • •	• • • •
CED-6		I E	R	L	A	Ē	Α	Ĺ	R A	N	S	K	Α	D	'Y
hCED-6		N K	v	Q	D	L	E	N	Q L	R	I	T	Q	V	S
	conconque	1001 AATAA	\	א א	יינט ע בֿי	TTCC	ממת	ארר	AACT	CAC	א ת <i>ת</i>	ACT	ሮ አ አ		1050 TCAG
	consensus pGA101	AATAA				TTGG			AACT						TCAG
	Seq	AATAA	AGTAC	A A	GAT'	TTGG	AAA	AACC	CAACT	GAG.	AATA	ACT	CAA	GTA'	TCAG
	oGA107	AATAA								•					
	oGA102 aa307982	AATAA AATAA		_								-			
	aa307962	AM I AM	AGIAC	A.A	JA 1	1100	AAA	MCC	.AACI	GAG.	MM 1 F	MCI	CAA	GIM	ICAG
CED-6		E N	T G	. P	•	P	I	Y	P	G	L	G	P	P	A
hCED-6		A P	P A	G		S	M	T	₽	K	S	P	S		D
	consensus	1051 CACCTO	ግሮልርሮ	AGG	$C\Delta$	GТ	ልጥር	מרמ	יררבז.	D.G	ፐርር	בררר	ፐሮሮ		1100 GAC
	pGA101	CACCT							CCTA						GAC
	Seq	CACCTO	CCAGC	AGG	CA	GT	ATG	BACA	CCTA	AG	TCG	CCC	TCC.	ACT	GAC
	oGA107	CACCTO							CCTA						GAC
	oGA102 aa307982	CACCTO													
	44307702	CACCI	.cncc,	, ,,,,,,,			7110	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		7,0.		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	.100		. 0710
CED-6	LPLSPM	-	G		P			I	P	P		S	I		S
hCED-6		I F	D	M	I	Þ	F	S	P	I	S	H	Q		S 1150
	consensus	1101 ATCTT	rgata	. TGI	ATT(CCAT	TTT		TCCA	ATA	T.CA	CAC	Ċ.A		
	pGA101	ATCTT				CCAT			TCCA						
•	Seq	ATCTT		_		CCAT			TCCA				_		
	OGA107 OGA102	ATCTT:				CCAT			TCCA						
•	aa307982	ATCTT							CC						
. •	aa443368				(CCAT	TTT	CT	CC	AA'	TATO	CACA	CCA	GTC'	TTC.
CED C			. 15	,	x 1	3.7	·	7	n		er.	TO.	3.6		.
CED-6 hCED-6		• 7	PR PT			N N	D G	L T	P Q	P P	· T P	· E P	M V	A P	Ś
	•	1151		-		•		-	=	_		-	• •		1200
	consensus	GATGC	CTAC.	.TC	GCA	AT	GGC	CACA	CAGC						
	nCN101	CATCC	ጉጥ አ ርጉ	ጥርረ	<u>ግ</u> ሮ Λ '	אמיי	GG C	מי <i>ם</i> מי	CAGC						13-R
	pGA101 Seq	GATGC			GCA. GCA.				CAGC				•	_	_
	oGA107	GATGC			GCA				CAGC						
	oGA102	GATGC				ATTG			CAGC						_
•	aa307982	GATGC				AT			CAGC						
	aa443368 aa431995	GATGC	· IMC ·	TCG(T AGTC			CAGC						
				**	 • •		, * *				• •		_ •••		
CED-6		T L	P Q		S		S	S	N		A S		S	V	
hCED-6		R'S	T E	·I	K	R	D	L	F	G	A E	Е Р	F	D	P 1250
	consensus	1201 <u>GAT</u> CT/	ACTGA	GAT'	TAA.	ACGG	GAC	CTC	TTTG	GAG	CAGA	ACC	TTT		
•		GATCT!											•		

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	MO 1 1-		- 1 <i>5</i>	156		
	F1G. 1. 100			·	CACCACAACC	TTTC > CCC>
	Seq oGA107		GATTAAANGG GATTAAANGG			
	oGA102 aa443368		GATTAAACGG	GACCTGTTTG	GAGCAGAACC	TTTTGACCCA
	aa431995	ATCAAAGCAT	GAATATTTCA	ACTTTAGTGT	TCACTGATTT	TATTTTGCTG
CED-6		P A S	T S P S	G P A	P S I	P P P A
hCED-6		F N C	G A A D	F P P	D I Q	S K L D 1300
•	consensus	1251 TTTAACTGTG	GAGCAGCAGA	TTTCCCTCCA	GATATTCAAT	
		•	Primer oGA1	<u> </u>		
	pGA101	TTTAACTGTG	-		GATATTCAAT	
	Seq	TTTAACTGTG	•		GATATTCAAT	
	oGA107 aa443368				GATATTCAAT	
	aa431995	TAACATTT			GATATTAATT	
CED-6		STS	P S G	P A P S	I P P	PRP
hCED-6		E M Q	E G F	K M G L	TLE	G T V
	concencus	1301	GAGGGGTTCA	አአአ ጥርርርአርጥ	אוריים	1350 GCACAGTAT
	consensus pGA101	TGAGATGCAG			AACTCTTGAA	•
	Seq	TGAGATGCAG			AACTCTTGAA	
	oGA107	TGAGATGCAG	GAGGGGTTCA	AAATGGGACT	AACTCTTGAA	GGCACAAGTAT
	oGA108	-	GAGGGGTTCA			•
	aa443368		GAGGGGTTCA	•		•
	aa431995	GIIIIA.CAG	GAGGGGTTCA	AAAIGGGACI	AACICIIGAA	GGCACAGIAI
CED-6		P A L A	P P P	P V A		
hCED-6		F C L D	P L D	S R C	, ★	
. •		1351				1400
	consensus	TTTGTCTCGA	CCCGTTAGAC	-	GACATCAAGA 445-10934-	
	Seq	TTTGTCTCGA			GACATCAAGA	
	oGA107	TTTGTCTCGA	,		GACATCAAGA	•
• •	oGA108 aa443368	TTTGTCTCGA TTTGTCTCGA		AGTAGGTGCT	GACATCAAGA GACATCAAGA	
, -	aa431995	TTTGTCTCGA	•		GACATCAAGA	•
					•	
CED-6 CED-6	PRRNPVVS PKNST. SFDPRAGEKK STA KKTAAEYDAM INE	AEYNPFG ADFI	LSGIQNG KEA	PPSASAE LLAS		·
		7.4.0.1				1450
- .	consensus	1401 CTGATTCATG	ጥጥል ል ልጥርጥርጥ	-	САТСТСАТТТ	1450 ATTATTATTA
·	Consciisas		oGA109-F	<u> </u>		
•	Seq		TTAAATGTGT	TTGTATAC A	CATGTCATTT	ATTATTATTA
•	oGA107	CTGATTCATG	TTAAATGTGT	TTGTATAC A	•	
	oGA109	0m03.mm03.==	mmaaamaaa	mmamama a a	ACTGTTCATT	•
	oGA108 aa443368	CTGATTCATG CTGATTCATG			CATGTCATTT	•
	aa431995	CTGATTCATG			CATGTCATTT	
	r33389	CTGATTCATG			CATGTCATTT	
						•
•		1451		armamama:	- -	1500
	consensus		GGTATTA TT		TGTTTTTGAA	
	Seq oGA107	CTTTAAGATA	GGTATTA TT	· · ·	TGTTTTTGAA TGGTTTTTTGA	
	oGA107	CTTTANNAA	GGTTATTATT		GNTTTTNTAA	
	oGA108	CTTTAAGATA			TGTTTTTGAA	
•	aa443368		GGTATTA TT	•	TGTTTTTGAA	TATTTTAATA
•		SUBST	TITUTE SHEE	T (RULE 26)		

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FIG	1. (CONTII	VUED)	0100		
,,,,,,	. (00000				
aa431995	CTTTAAGATA	GGTATTA TT	CATGTGTCAA	TGTTTTTGAA	TATTTTAATA
r53881					GATA
r62236	AAGATA	GGTATTA.TT	CATGTGTCAA		TATTTTAATA
h03749	TAAGATA	GGTATTA.TT	CATGTGTCAA	TGTTTTTGAA	TATTTTAATA
r33389	CTTTAAGATA	GGTATTA.TT	CATGTGTCAA	TGTTTTTGAA	TATTTTAATA
•	1501				1550
consensus		TTTCTCAGTT	•	·	CACTATTGAT
Seq	"	TTTCTCAGTT	AAATTTCCT	CACCT T	CACTATTGAT
oGA109	TTTNTAAAAT	TTTCTCANTT	AAATTTCCT	CACCT T	CACTATTNNAT
oGA108	TTTTGAAAAT	TTTCTCAGTT	AAATTTCCT	CACCT T	CACTATTGAT
aa443368	TTTTGAAAAT	TTTCTCAGTT	AAATTTCCT	CACCT T	CACTATTGAT
aa431995	TTTTGAAAAT	TTTCTCAGTT	AAATTTCCT	CACCT T	CACTATTGAT
r53881	TTTTGAAAAT	TTTCTCAGTT	AAATTTCCT.	CACCTT	CACTATTGAT
r62236	TTTTGAAAAT	TTTCTCAGTT	AAATTTCCT.	CACCTT	
h03749	TTTTGAAAAT	TTTCTCAGTT	AAATTTCCT.		CACTATTGAT
r33389	TTTTGAAAAT	TTTCTCAGTT	AAATTTCCT.	CACCI	CACTATTGAT
	1661				1600
concencue	1551 CTGTAATTTT	ጥ አጥጥጥጥ እ እ እ እ	እርአርርም <u>ሞ</u> እርም	GTAAAGT	
consensus	CIGIAATITI	IAIIIIAAAA			934-03-R
Seq	CTGTAATTTT	ጥ አጥጥጥጥ አ አ አ አ	ACAGCTTACT		AGA TCATA
oGA109	CGTTAATTTT	TATTTTAAAA	ACNTCTTACN	T TAANTT	NNA TCATA
oGA103	CTGTAATTTT		ACAGCTTACT	G TAAAGT	AGA TCATA
aa443368	CTGTAATTTT		ACAGCTTACT	GT	non icaia
aa431995	CTGTAATTTT		ACAGCTTACT	G TAAAGT	AG A TCATA
r53881	CTGTAATTTT		ACAGCTTACT		AG. A. TCATA
r62236	CTGTAATTTT		ACAGCTTACT	• • •	AG.A.TCATA
h03749	CTGTAATTTT		ACAGCTTACT	· · · · · · · · · · · · · · · · · · ·	AG.A.TCATA
r33389	CTGTAATTTT			GTAAAGT	AGGA.TCATA
	1601				1650
consensus	CTTTT ATG	TTCCTTTCTG	TTTCTACTGT	AGATGAAT	TTGTAATTGA
Seq	CTTTT ATG	TTCCTTTCTG	TTTCTACTGT	AGAT GAAT	TTGTAATTGA
oGA109	CTTTT ANN	TTCCTTTCGA	TTTCTACGC	TNNA GNAA	TTGNTAATTATA
oGA108	CTTTT ATG	TTCCTTTCTG	TTTCTACTGT	AGAT GAAT	TTGTAATTGA
aa431995	CTTTT ATG	TTCCTTTCTG	TTTCTACTGT	AGAT GAAT	TTGTAATTGA
r53881	CTTTTATG	TTCCTTTCTG	TTTCTACTGT	AGATGAAT	TTGTAATTGA
r62236	CTTTTATG	TTCCTTTCTG	TTTCTACTGT	AGATGAAT	TTGTAATTGA
h03749		- -		AGATGAAT	*···.
r33389	CTTTTATG	TTCCTTTCTG	TTTCTACTGT	AGGATGGAAT	TTGTAATTGG
	1651				1700
consensus	AAG.ACATAT	TATACAAATA	* - *A	4	CTATTTAGTT
a	110 101m		cimer 445-10		CM s comm s comm
Seq		TATACAAATA			
oGA109	ANT ACATAT	TATACAAATA	-		CTATTTATTT
oGA108	AAG ACATAT	TATACAAATA	•	GTCTGAG TT	
aa431995	AAG ACATAT	TATACAAATA		GTCTGAG TT	•
r53881	AAG.ACATAT	TATACAAATA		GTCTGAG.TT	
r62236	AAG.ACATAT	TATACAAATA			
h03749	AAG.ACATAT	TATACAAATA		GTCTGAGGTT	
r33389	AAGGACATAT	TATACAAATA	CCIGCCIIGI	GICIGAGGII	CIATIAGGIA
•	1701		•		1750
consensus		AAATTT <u>GTAT</u>	ייר <i>א</i> יייירר א	GATGGGTAGT	•
COMPENDUS	AGC ATCTTG		cimer oGA110		IINIIMAIUM
Seq	AGC ATCTTG			GGATGGCTAGT	ተ ተልተ ተል ል ጥር ል
oGA109	NTC ATCTGT	_	TCATTTTCCA	•	TTATTAAGNAT
oGA103		AAATTGATAT	•	•	•
oGA110		,			CTTTAATGA
	SUI	BSTITUTE SE	EET (RULE	·	

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FIG.	1. (CONTI	INUED)	1100		
r53881	-		TCATTTTCCA	GATGGCTAGT	TTATTAATGA
r62236		AAATTTGTAT	TCATTTTCCA	·	TTATTAATGA
h03749	AGC.ATCTTG	AAATTTGTAT	TCATTTTCCA	GATGGCTAGT	TTATTAATGA
r33389	GGCCATCTGG	AAATTTGTAT	TCATT		
	1751		-		1800
consensus	TTTCCCAAAA	GCCATACCTT	AAAG.ATAAC	TTTTTAAATT	CTGAAGAG
		•		primer 445-	<u>-10934-12-R</u>
Seq	TTTCCCAAAA	GCCATACCTT	AAAG ATAAC	TTTTTAAATT	CTGAAGA G
oGA109	TTCCCAAAN I	CCATACCTT	AANT ATAAC	TTTTTAAATT	TNTAATA T
oGA108	TTTCCCAAAA	GCCATACCTT	AAAG ATAAC	TTTTTAAATT	CTGAAGA G
oGA110	- · · ·	GCCATACCTT	AAAG ATAAC	TTTTTAAATT	CTGAAGA G
r53881	TTTCCCAAAA		AAAG.ATAAC		
r62236	TTTCCCAAAA				CTGGAAGA.G
h03749	TTTCCCAAAA	GCCATACCTT	AAAGGATAAC	IIIIIAAAII	CIGGAAGGNG
••	1801		•		1850
consensus	<u>ACATGCCAAT</u>	<u>G</u> TCAAACTAA	ACATGTTCTG	TTTTTAAA.C	•
Seq	ACATGCCAAT			TTTTTAAA C	F
oGA109	ACANTCCAA C	•	·		CAACAAACAN
oGAI10	ACATGCCAAT			TTTTTAAA C	
oGA108	· · · · · · · · · · · · · · · · · · ·	GTCAAACTAA			CAACAAACAT
r53881	· · · · ·	GTCAAACTAA		TTTTTAAA.C	
r62236		GTCAAACTAA	ACATGTTCCG	TTTTTAAAAC	
h03749	ACATGCCAAT	GICAAACIAA	ACAIGITCCG	TITITAAAC	CAACAAACAI
	1851				1900
consensus	GTTA.CTATT	CATTGG.ACA	GATATCATTT	TATGTATA	AATACTGTT.
Seq	GTTA CTATT	CATTGG ACA	GATATCATTT	TATG TATA	AATACTGTT
oGA109	NTTA CTATT	CATGNGNACA	NATATCATTT		AACACTANT
oGA108	GTTA CTATT	CATTGG ACA		NATG TATA	•
oGA110	GTTA CTATT	CATTGG ACA	GATATCATTT		AATACTGTT
r53881	GTTA.CTATT	CATTGGGACA	GNTATCCTTT	TATGGTATTA.	AATACTGTTC
r62236	GTTAACTATT	TCATGGGACA	• • • • • • • •		
h03749	GTTA.CTATT	TCAIG			• • • • • • • • •
	1901		·		1950
consensus			AAACTTT.AA	•	_
Seq	CACATCACTG	_	AAACTTT AA		•
oGA109	TCACATCACTO			-	CACANGTTCAC
oGA110	CACATCACTG	G GAAAATGT	AAACTTT AA		•
r53881	CACCTCACCG	GGGGNATGGT	AAACCTTNAA	ACCINATEGC	CNCAGGGGCA
	1951	, , , , , , , , , , , , , , , , , , ,		•	2000
consensus	TAATTTCTAG	CAGGTAAAAT	TATAAGGATA	TAAATTCCAA	TAATAAACCA
Seq	TAATTTCTAG	CAGGTAAAAT	TATAAGGATA	TAAATTCCAA	TAATAAACCA
oGA109	TAATTTCTAA	CNGATNAAAT			TAATAAACCCA
oGA110	TAATTTCTAG	CAGGTAAAAT	TATAAGGATA		
aa431753rcc		GGTAAAAT	TATAAGGATA	TAAATTCCAA	TAATAAACCA
r53881	CCNTTTTNCG	GCG	• • • • • • • •	• • • • • • • •	
	2001	,			2050
consensus	AATGTATTTA	GAGTATTTAT		AAGGTGATGT	
,	•			orimer 445-1	
		:	•	imer 445-109 AGGTGATGGTT	
pGA101	እ አመረተው አመጣጥ አ	ር! እ ርግጥ እ ጥጥጣ ኦ ጥ		AAGGTGATGT AAGGTGATGT	
Seq oGA109	AATGTATTTA	GAGTATTTAT AGAATATTTAT?		CAGNTGAA	MATHIORE
oGA110	AATGTATTTA			AAGGTGATGT	TAGTTATGAT
aa431753rcc			- ·	·	
aa159297rcc					GATGAT
· ·			EET (DIN E 1		

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FIG. 1. (CONTINUED) 8/56

	2051				2100
consensus	CAGTTATACT	CTAAATATTT	AATTTGTTTT	ATAAAGGTAG	TGAAAAAATG
pGA101 CA	GGTTAAAACCT(CTAAAATATTNA	AATNTTGTTTT	ATAAAGGTAG	GAAAAAATG
Seq	CAGTTATACT	CTAAATATTT	AATTTGTTTT	ATAAAGGTAG	TGAAAAAATG
oGA110	CAGTTATACT	CTAAATATTT	AATTTGTTTT	ATAAAGGTAG	TGAAAAAATG
aa431753rcc	CAGTTATACT	CTAAATATTT	AATTTGTTTT	ATAAAGGTAG	TGAAAAAATG
aa159297rcc	CAGTTATACT	CNAAATATTN	AATTTGTNTT	ATAAAGGTAG	TGAAAAAATG
aa770228rcc	TATACT	CTAAATATTT	AATTTGTTTT	ATAAAGGTAG	TGAAAAAATG
h02853rcc	IAIACI	CIMMINITI	T	ATAAGGGTAG	NGAAAAAANG
1102033100	• • • • • • • • •		,	111111111111111111111111111111111111111	, ,
•	2101			•	2150
	AAAATTTGCT	አ መመመስ መመለ አ አ	AAACATTAAA	· ጥጥጥር! - አ ጥጥር ር!	AAATGAGAT
consensus	AAAATTIGCT	ATTIATTAAA	AAACAI IAAA	·/-	
CIN 1 O 1	* * * * * *********************	3 mmm 3 mm 3 3 3	እ እ አ <i>ረግ</i> እ መጠ እ እ እ	primer 445-	
pGA101	AAAATTTGCT		AAACATTAAA		AAATGAGAT
Seq	AAAATTTGCT	ATTTATTAAA	AAACATTAAA	•	AAATGAGAT
oGA110	AAAATTTGCT	ATTTATTAAA	AAACATTAAA		AAATGAGAT
aa431753rcc	AAAATTTGCT	ATTTATTAAA	AAACATTAAA	•	AAATGAGAT
aa159297rcc	AAAATTTGCT	ATTTATTAAA	AAACATTAAA	TTTC.ATTCC	AAATGAGAT
aa770228rcc	AAAATTGGCT	ATTTATTAAA	AAACATTGAA	TTTC.ATTCC	AAATGAGAT
h02853rcc	AAAATTNGCT	ATTTATTAAA	AAACATTAAA	TTTC.ATTCC	CAAATGAGAT
d60819rcc	• • • • • • • • • •	. ATTATKRAA	AAACATTAAA		.AAATGAGAT
r62135rcc			AAACATTAAA	TGTCCANGCC	CAAATGAGAT
	2151	•	•		. 2200
consensus	AAGTG.ATAT	TAC.TATAAC	ATC. TAAGCA	TCATCTGA	TTTG.ATATT
pGA101	AAGTG ATAT	TAC TATAAC	ATC TAAGCA	TCATCT GA	TTTG ATATT
Seq	AAGTG ATAT	TAC TATAAC	ATC TAAGCA	TCATCT GA	TTTG ATATT
oGA110	AAGTG ATAT	TAC TATAAC	ATC TAAGCA	TCATCT GA	TTTG ATATT
aa431753rcc	AAGTG.ATAT	TAC.TATAAC	ATC. TAAGCA	TCATCTGA	TTTG.ATATT
aa159297rcc	AAGTG.ATAT	TAC.TATAAC	ATC.TAAGCA	TCATCTGA	TTTG.ATATT
aa770228rcc	AAGTG.ATAT	TAC.TATAAC	ATC.TAAGCA	TCATCTGA	TTTG.ATATT
h02853rcc	AAGTG.ATAT	TACCTATAAC	ATCCTAAGCA	TCATCTGA	TTTG.ATANT
d60819rcc	AAGTG.ATAT	TAC.TATAAC	ATC.TAAGCA	TCATCTGA	TTTG.ATATY
r62135rcc	AAGTGGATAN	TACCTATAAC	ATCCTAAGCA	TCATCCTGNA	TTTGNANANT
	•	•			
	2201				2250
consensus	CCCT. AAAAA	ACATTTGGAA	TATATGCTAT	CTATAGATTC	AGTATCTACT
pGA101	CCCT AAAAA	ACATTTGGAA	TATATGCTAT	CTATAGATTC	AGTATCTACT
Seq	CCCT AAAAA	ACATTTGGAA	TATATGCTAT	CTATAGATTC	AGTATCTACT
oGA110	CCCT AAAAA	ACATTTGGAA	TATATGCTAT	CTATAGATTC	AGTATCTACT
aa431753rcc	CCCT AAAAA	ACATTTGGAA	TATATGCTAT	CTATAGATTC	AGTATCTACT
aa159297rcc	CCCT.NAAAA	ACATTTGGAA	TATATGCTAT	CTATAGATTC	AGTATCTACT
aa770228rcc	CCCT. AAAAA	ACATTTGGAA	TATATGCTAT	CTATAGATTC	AGTATCTACT
h02853rcc			TATATGCTAT	* **	
d60819rcc			TATATGCTAT		•
r62135rcc		ACATTTGGNA	•	CTATAGATTC	
				•	
•	2251				2300
consensus		ACTTTACC.A	AATATATTTC	TCCTCACTGC	ATAAGGACTA
pGA101			AATATATTTC	· ·	
Seq	ACCCATATTT		AATATATTTC		
oGA110	ACCCATATTT		AATATATTTC		_
aa431753rcc			AATATATTTC		•
aa159297rcc			AATATATTTC		•
aa770228rcc			AATATATTTC	•	
	$\Delta(\mathcal{A}(\mathcal{A}(\mathcal{A}))))$				
DID JAK ATOO					*
h02853rcc	ACCCATATTT	ACTTTACC.A	AATATATTTC	TCCTCACTGC	ATAAGGACTA
d60819rcc r62135rcc	ACCCATATTT ACCCATATTT	ACTTTACC.A ACTTTACSSA		TCCTCACTGC TCCTCACTGC	ATAAGGACTA ATAAGGACTA

FIG. 1. (CONTINUED)

• '				<u></u>	
consensus	CTCTTCTCAT	ATTTTCTTCT			CAAAGTTTAT
pGA101	CTCTTCTCAT	ATTTTCTTCT	TTGATGAAGA	TATTTTTCAC	CAAAGTTTAT
Seq	CTCTTCTCAT	ATTTTCTTCT	TTGATGAAGA	TATTTTTCAC	CAAAGTTTAT
oGA110	CTCTTCTCAT	ATTTTCTTCT	TTGATGAAGA	TATTTTTCAC	
aa431753rcc	CTCTTCTCAT	ATTTTCTTCT	TTGATGAAGA	TATTTTTCAC	CAAAGTTTAT
aa159297rcc	CTCTTCTCAT	ATTTTCTTCT	TTGATGAAGA	TATTTTTCAC	CAAAGTTTAT
aa770228rcc	CTCTTCTCAT	ATTTTCTTCT	TTGATGAAGA	TATTTTTCAC	CAAAGTTTAT
h02853rcc	CTCTTCTCAT	ATTTTCTTCT	TTGATGAAGA	· -	CAAAGTTTAT
d60819rcc	CTCTTCTCAT	ATTTTCTTCT	TTGATGAAGA	TATTTTTCAC	CAAAGTTTAT
r62135rcc	CTCNTCTCAT	ATTTTCTTCT	TTGATGAAGA	TATTTTTCAC	CAAAGTTTAT
			•		
	2351				2400
consensus	TTTGTGATGC	CCTCTTGGTT	TTGATACTTT	AAAATCTGTG	GCACCCGTTC
pGA101	TTTGTGATGC	CCTCTTGGTT	TTGATACTTT	AAAATCTGTG	GCACCCGTTC
Seq	TTTGTGATGC	CCTCTTGGTT	TTGATACTTT	AAAATCTGTG	GCACCCGTTC
oGA110	TTTGTGATGC	CCTCTTGGTT	TTGATACTT A	AAAAATCTGTG	GCACCCGTTC
aa431753rcc	TTTGTGATGC	CCTCTTGGTT	TTGATACTTT	AAAATCTGTG	GCACCCGTTC
aa159297rcc	TTTGTGATGC	CCTCTTGGTT	TTGATACTTT	AAAATCTGTG	GCACCCGTTC
aa770228rcc	TTTGTGATGC	CCTCTTGGTT	TTGATACTTT	AAAATCTGTG.	GCACCCGTTC
h02853rcc	TTTGTGATGC	CCTCTTGGTT	TTGATACTTT	AAAATCTGTG	GCACCCGTTC
d60819rcc	TTTGTGATGC	CCTCTTGGTT	TTGATACTTT	AAAATCTGTG	GCACCCGTTC
r62135rcc	TTTGTGATGC	CCTCTTGGNT	TTGATACTTT	AAAATCTGTG	GCACCCGTTC
					•
	2401				2450
consensus	TACATGAATT	ATCAATATTT		ATCTGTATTT	GTTTTGTTAA
pGA101	TACATGAATT	ATCAATATTT	GGTAAATTCA	ATCTGTATTT	GTTTTGTTAA
Seq	TACATGAATT	ATCAATATTT	GGTAAATTCA	ATCTGTATTT	GTTTTGTTAA
oGA110	TACATGAATT	ATCAATATTT	GGTAA TTCA	ATCTGTATTT	GTTTGGTAAA
aa431753rcc	TACATGAATT	ATCAATATTT	GGTAAATTCA	ATCTGTATTT	GTTTTGTTAA
aa159297rcc	TACATGAATT	ATCAATATTT	GGTAAATTCA	ATCTGTATTT	GTTTTGTTAA
aa770228rcc	TACATGAATT	ATCAATATTT	GGTAAATTCA	ATCTGTATTT	GTTTTGTTAA
h02853rcc	TACATGAATT	ATCAATATTT	GGTAAATTCA	ATCTGTATTT	GTTTTGTTAA
d60819rcc	TACATGAATT	ATCAATATTT	GGTAAAKTCA	ATCTGTATTT	GTTTTGTTAA
r62135rcc	TACATGNATT	ATCAATATTT	GGTAAATTCA	ATCTGTATTT	GTTTTGTTAA
	2.451				2498
consensus	AGTCAAAAAT	CTCATTTTCC	• • • • • • • • •	• • • • • • • • • •	• • • • • • • • • •
pGA101	AGTCAAAAAT	CTCATTTTCC	AGTCGACGCG	GCCGC	
Seq	AGTCAAAAAT	CTCATTTTCC	AAAAAAAAA	AAAAAAAACT	CGAG
oGA110	ATCCAAAAATN	INNCATT			
aa431753rcc	AGTCAAAAAT	CTCATTTTCC	AAAA	• • • • • • • • • •	• • • • • • •
aa159297rcc	AGTCAAAAAT	CTCATTTTCC			• • • • • • •
aa770228rcc	AGTCAAAAAT	CTCATTT	• • • • • • • • • •		
h02853rcc	AGTCAAAAAN	NTCAANNTCC			
d60819rcc	AGTCRAAAAT				
r62135rcc	AGTNANNANT	CTCATTTTCC	AANANGGGGG	GGGGGGGGA	AGTTCCTG
	•				

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F1G. 2.

GGTGATGAGCCCTTGGGTTCTCGCTCCGACTGCTAAATTCGCTTGGCCGGGTCCACCTTCTCGTGGCCT CACTCGCCACACGGATCAGAATCCGGAGCAGGCAGTTCTCTCTATTCTGAGGCTCCTGCGGCTGCCGCG CTGACTTCCCTGTGTGGNGGAGGGAACTCTGGGCAGGCTGGTTTTCTTGGAATGTGTTTACGATGTTGA TGATATACATAGGAGAGAAACTGATAGAAGAATTCTGATGGCAACTGTATGATAGAAGCTATATAAAG TCAAGTGTCCATTTTCTTTCAACTATATTTGAGCATACCCAGGATTTAAGTCGTGGAACTGAACATTTAT TTGGCTGATCCTCATCATGAACCGTGCTTTTAGCAGGAAGAAAAGACAAAACATGGATGCATACACCTG AAGCTTTATCAAAACATTTCATTCCCTATAATGCAAAGTTTCTTGGCAGTACAGAAGTGGAACAGCCAA AAGGAACAGAAGTTGTGAGAGATGCTGTAAGGAAACTAAAGTTTGCAAGACATATCAAGAAATCTGA AGGCCAGAAAATTCCTAAAGTGGAGTTGCAAATATCAATTTATGGAGTAAAAATTCTAGAACCCAAAA CAAAGGAAGTTCAACACAATTGCCAGCTTCATAGAATATCTTTTTGTGCAGATGATAAAACTGACAAG **AGGATATTCACTTTCATATGCAAAGATTCTGAGTCAAATAAACATTTGTGCTATGTATTTGACAGCGAA** <u>AAGTGTG</u>CTGAAGAGATCACTTTAACAATTGGCCAAGCATTTGACCTGGCATACAGGAAATTTCTAGA ATCAGGAGGAAAAGATGTTGAAACAAGAAAACAGATCGCAGGGTTACAAAAAAGAATCCAAGACTTA GAAACAGAAAATATGGAACTTAAAAAATAAAGTACAAGATTTGGAAAAACCAACTGAGAATAACTCAAG TATCAGCACCTCCAGCAGCAGTATGACACCTAAGTCGCCCTCCACTGACATCTTTGATATGATTCCAT TTTCTCCAATATCACACCAGTCTTCGATGCCTACTCGCAATGGCACACAGCCACCTCCAGTACCTAGTA GATCTACTGAGATTAAACGGGACCTGTTTGGAGCAGAACCTTTTGACCCATTTAACTGTGGAGCAGCA TGAAGGCACAGTATTTTGTCTCGACCCGTTAGACAGTAGGTGCTGACATCAAGAACAAGAAATCCTGA TTCATGTTAAATGTGTTTGTATACACATGTCATTTATTATTATTATTACTTTAAGATAGGTATTATTCATGTG TCAATGTTTTTGAATATTTTTGAAAATTTTCTCAGTTAAATTTCCTCACCTCACCTATTGATCT GTAATTTTTAAAAAACAGCTTACTGTAAAGTAGATCATACTTTTATGTTCCTTTCTGTTTCTACTGT ATCTTGAAATTTGTATTCATTTTCCAGATGGCTAGTTTATTAATGATTTCCCAAAAGCCATACCTTAAAG ATAACTTTTTAAATTCTGAAGAGACATGCCAATGTCAAACTAAACATGTTCTGTTTTTAAACCAACAAA CATGTTACTATTCATTGGACAGATATCATTTTATGTATAAATACTGTTCACATCACTGGGAAAAATGTAA **ACTITAAACATAATGCCACAAGGTCACTAATTTCTAGCAGGTAAAATTATAAGGATATAAATTCCAATA** TTTCATTCCAAATGAGATAAGTGATATTACTATAACATCTAAGCATCATCTGATTTGATATTCCCTAAA AAACATTTGGAATATATGCTATCTATAGATTCAGTATCTACTACCCATATTTACCTTACCAAATATATTT CTCCTCACTGCATAAGGACTACTCTTCTCATATTTTCTTCTTTTGATGAAGATATTTTTCACCAAAGTTTA TTTTGTGATGCCCTCTTGGTTTTGATACTTTAAAATCTGTGGCACCCGTTCTACATGAATTATCAATATT CTCGAG

F1G.3.

GGTGATGAGCCCTTGGGTTCTCGCTCCGACTGCTAAATTCGCTTGGCCGGGTCCACCTTCTCGTGGCCT CACTCGCCACACGGATCAGAATCCGGAGCAGGCAGTTCTCTCTATTCTGAGGCTCCTGCGGCTGCCGCG CTGACTTCCCTGTGTGGGGGGGGGGGGGCACTCTGGGCAGGCTGGTTTTCTTGGAATGTGTTTACGATGTTGA TGATATACATAGGAGAGAAACTGATAGAAGAATTCTGATGGCAACTGTATGATAGAAGCTATATAAAG TCAAGTGTCCATTTTCTTTCAACTATATTTGAGCATACCCAGGATTTAAGTCGTGGAACTGAACATTTÁT **AAGCTTTATCAAAACATTTCATTCCCTATAATGCAAAGTTTCTTGGCAGTACAGAAGTGGAACAGCCAA** AAGGAACAGAAGTTGTGAGAGATGCTGTAAGGAAACTAAAGTTTGCAAGACATATCAAGAAATCTGA AGGCCAGAAAATTCCTAAAGTGGAGTTGCAAATATCAATTTATGGAGTAAAAATTCTAGAACCCAAAA CAAAGGCTGAAGAGATCACTTTAACAATTGGCCAAGCATTTGACCTGGCATACAGGAAATTTCTAGAA AAACAGAAAATATGGAACTTAAAAAATAAAGTACAAGATTTGGAAAAACCAACTGAGAATAACTCAAGT ATCAGCACCTCCAGCAGCAGTATGACACCTAAGTCGCCCTCCACTGACATCTTTGATATGATTCCATT TTCTCCAATATCACACCAGTCTTCGATGCCTACTCGCAATGGCACACAGCCACCTCCAGTACCTAGTAG ATCTACTGAGATTAAACGGGACCTGTTTGGAGCAGAACCTTTTGACCCATTTAACTGTGGAGCAGCAG ATTTCCCTCCÄGATATTCAATCAAAATTAGATGAGATGCAGGAGGGGTTCAAAATGGGACTAACTCTT GAAGGCÄCÄGTATTTTGTCTCGACCCGTTAGACAGTAGGTGCTGACATCAAGAACAAGAAATCCTGAT TCATGTTAAATGTGTTTTGTATACACATGTCATTTATTATTATTATTACTTTAAGATAGGTATTATTCATGTGT CAATGTTTTTGAATATTTTGAAAATTTTCTCAGTTAAATTTCCTCACCTTCACTATTGATCTG TAATTTTAATTTTAAAAACAGCTTACTGTAAAGTAGATCATACTTTTATGTTCCTTTCTGTTTCTACTGTA TCTTGAAATTTGTATTCATTTTCCAGATGGCTAGTTTATTAATGATTTCCCAAAAGCCATACCTTAAAGA TAACTTTTTAAATTCTGAAGAGACATGCCAATGTCAAACTAAACATGTTCTGTTTTTAAACCAACAAAC ATGTTACTATTCATTGGACAGATATCATTTTATGTATAAATACTGTTCACATCACTGGGAAAATGTAAA CTTTAAACATAATGCCACAAGGTCACTAATTTCTAGCAGGTAAAATTATAAGGATATAAATTCCAATAA TTCATTCCAAATGAGATAAGTGATATTACTATAACATCTAAGCATCATCTGATTTGATATTCCCTAAAA AACATTTGGAATATATGCTATCTATAGATTCAGTATCTACTACCCATATTTACCTATCCAAATATATTTC TCCTCACTGCATAAGGACTACTCTTCTCATATTTTCTTCTTTGATGAAGATATTTTTCACCAAAGTTTAT TTTGTGATGCCCTCTTGGTTTTGATACTTTAAAATCTGTGGCACCCGTTCTACATGAATTATCAATATTT **TCGAG**

F1G. 4.

MNRAFSRKKDKTWMHTPEALSKHFIPYNAKFLGSTEVEQPKGTEVVRDAVRKLKFARHIKKS EGQKIPKVELQISIYGVKILEPKTK<u>EVQHNCQLHRISFCADDKTDKRIFTFICKDSESNKHLCYV</u> <u>FDSEKC</u>AEEITLTIGQAFDLAYRKFLESGGKDVETRKQIAGLQKRIQDLETENMELKNKVQDLE NQLRITQVSAPPAGSMTPKSPSTDIFDMIPFSPISHQSSMPTRNGTQPPPVPSRSTEIKRDLFGAEP FDPFNCGAADFPPDIQSKLDEMQEGFKMGLTLEGTVFCLDPLDSRC*

F1G.5.

MNRAFSRKKDKTWMHTPEALSKHFIPYNAKFLGSTEVEQPKGTEVVRDAVRKLKFARHIKKS EGQKIPKVELQISIYGVKILEPKTKAEEITLTIGQAFDLAYRKFLESGGKDVETRKQIAGLQKRIQ DLETENMELKNKVQDLENQLRITQVSAPPAGSMTPKSPSTDIFDMIPFSPISHQSSMPTRNGTQPP PVPSRSTEIKRDLFGAEPFDPFNCGAADFPPDIQSKLDEMQEGFKMGLTLEGTVFCLDPLDSRC*

F1G.6.

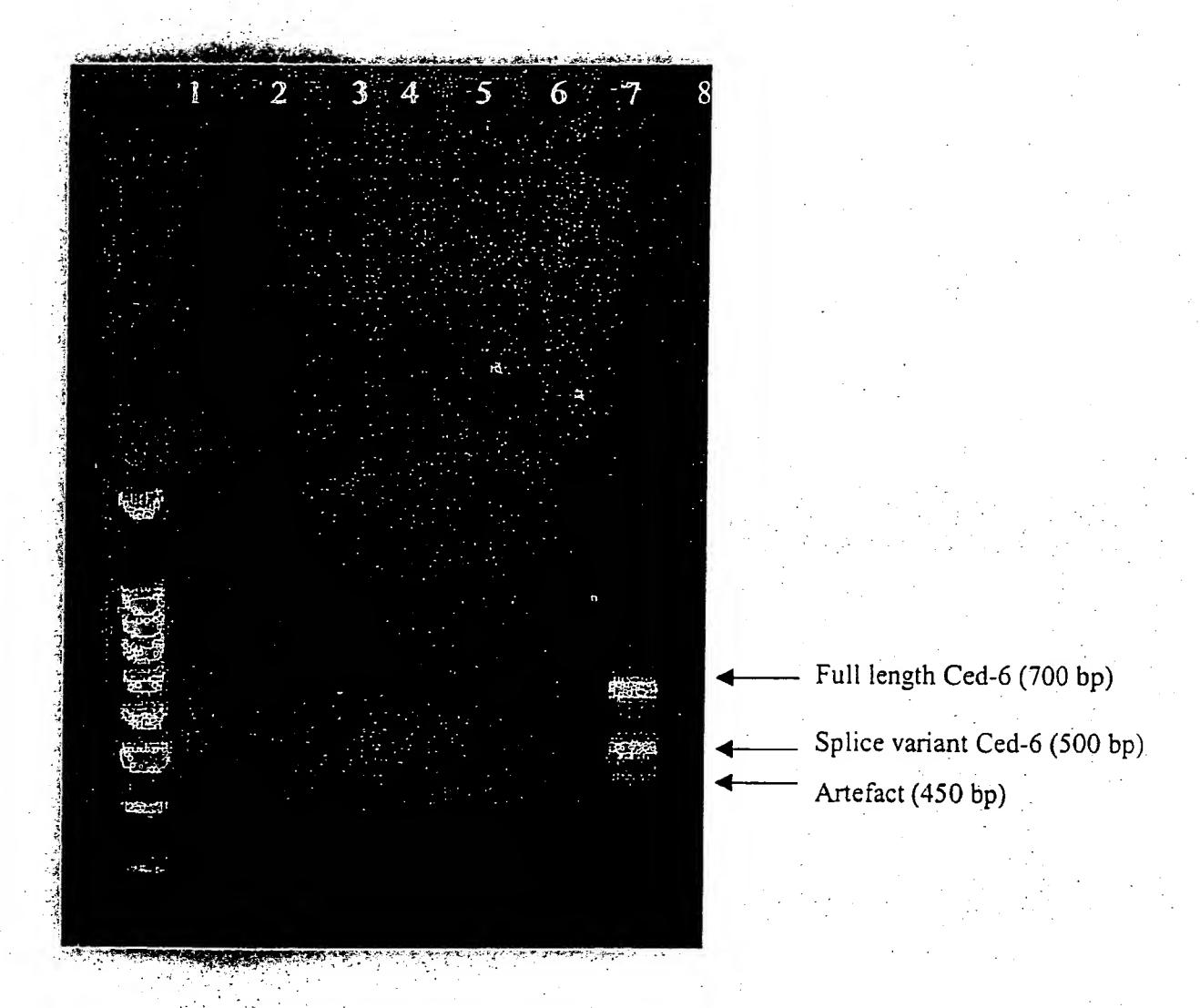


FIG. 7. 14/56

SQ SEQUENCE 4729 BP TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA TGGAGTTCCG 60 CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCCGCCCATT 120 GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC ATTGACGTCA 180 ATGGGTGGAG TATTTACGGT AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC 240 AAGTACGCCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA 300 CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC 360 CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG 420 ATTTCCAAGT CTCCACCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC AAAATCAACG 480 GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT 540 ACGGTGGGAG GTCTATATAA GCAGAGCTGG TTTAGTGAAC CGTCAGATCC GCTAGCGCTA 600 CCGGACTCAG ATCTCGAGCT CAAGCTTCGA ATTCTGCAGT CGACGGTACC GCGGGCCCGG 660 GATCCATCGC CACCATGGTG AGCAAGGGCG AGGAGCTGTT CACCGGGGTG GTGCCCATCC 720 TGGTCGAGCT GGACGGCGAC GTAAACGGCC ACAAGTTCAG CGTGTCCGGC GAGGGCGAGG 780 GCGATGCCAC CTACGGCAAG CTGACCCTGA AGTTCATCTG CACCACCGGC AAGCTGCCCG 840 TGCCCTGGCC CACCCTCGTG ACCACCCTGA CCTACGGCGT GCAGTGCTTC AGCCGCTACC 900 CCGACCACAT GAAGCAGCAC GACTTCTTCA AGTCCGCCAT GCCCGAAGGC TACGTCCAGG 960 AGCGCACCAT CTTCTTCAAG GACGACGGCA ACTACAAGAC CCGCGCCGAG GTGAAGTTCG 1020 AGGGCGACAC CCTGGTGAAC CGCATCGAGC TGAAGGGCAT CGACTTCAAG GAGGACGGCA 1080 ACATCCTGGG GCACAAGCTG GAGTACAACT ACAACAGCCA CAACGTCTAT ATCATGGCCG 1140 ACAAGCAGAA GAACGGCATC AAGGTGAACT TCAAGATCCG CCACAACATC GAGGACGGCA 1200 GCGTGCAGCT CGCCGACCAC TACCAGCAGA ACACCCCCAT CGGCGACGGC CCCGTGCTGC 1260 TGCCCGACAA CCACTACCTG AGCACCCAGT CCGCCCTGAG CAAAGACCCC AACGAGAAGC 1320 GCGATCACAT GGTCCTGCTG GAGTTCGTGA CCGCCGCCGG GATCACTCTC GGCATGGACG 1380 AGCTGTACAA GTAAAGCGGC CGCGACTCTA GATCATAATC AGCCATACCA CATTTGTAGA 1440 GGTTTTACTT GCTTTAAAAA ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAAATGAA 1500

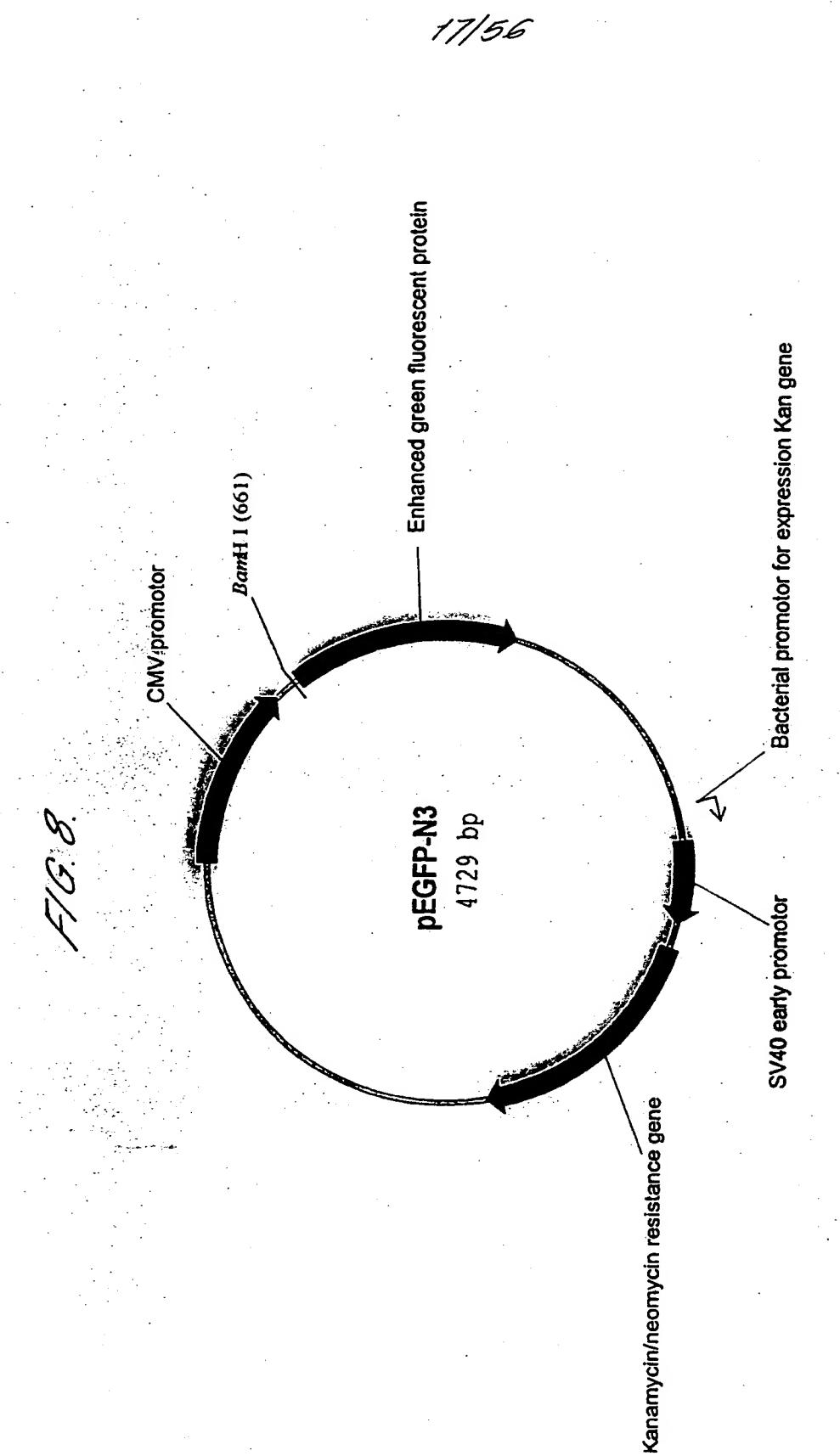
15/56 FIG. T. (CONTINUED)

1500		GTTGTTAACT	TGTTTATTGC	AGCTTATAAT	GGTTACAAAT	AAAGCAATAG
1560	CATCACAAAT	TTCACAAATA	AAGCATTTTT	TTCACTGCAT	TCTAGTTGTG	GTTTGTCCAA
1620	ACTCATCAAT	GTATCTTAAG	GCGTAAATTG	TAAGCGTTAA	TATTTTGTTA	AAATTCGCGT
1680	TAAATTTTTG	TTAAATCAGC	TCATTTTTTA	ACCAATAGGC	CGAAATCGGC	AAAATCCCTT
1740	ATAAATCAAA	AGAATAGACC	GAGATAGGGT	TGAGTGTTGT	TCCAGTTTGG	AACAAGAGTC
1800		GAACGTGGAC	TCCAACGTCA	AAGGGCGAAA	AACCGTCTAT	CAGGGCGATG
1860	GCCCACTACG	TGAACCATCA	CCCTAATCAA	GTTTTTTGGG	GTCGAGGTGC	CGTAAAGCAC
1920	TAAATCGGAA	CCCTAAAGGG	AGCCCCCGAT	TTAGAGCTTG	ACGGGGAAAG	CCGGCGAACG
1980	TGGCGAGAAA	GGAAGGGAAG	AAAGCGAAAG	GAGCGGGCGC	: TAGGGCGCTG	GCAAGTGTAG
2040	CGGTCACGCT	GCGCGTAACC	ACCACACCCG	CCGCGCTTAA	TGCGCCGCTA	CAGGGCGCGT
2100	CAGGTGGCAC	TTTTCGGGGA	AATGTGCGCG	GAACCCCTAT	TTGTTTATTT	TTCTAAATAC
2160	ATTCAAATAT	GTATCCGCTC	ATGAGACAAT	AACCCTGATA	AATGCTTCAA	TAATATTGAA
2220	AAA GGAAGAG	TCCTGAGGCG	GAAAGAACCA	GCTGTGGAAT	GTGTGTCAGT	TAGGGTGTGG
2280	AAAGTCCCCA	GGCTCCCCAG	CAGGCAGAAG	TATGCAAAGC	ATGCATCTCA	ATTAGTCAGC
2340	AACCAGGTGT	GGAAAGTCCC	CAGGCTCCCC	AGCAGGCAGA	AGTATGCAAA	GCATGCATCT
2400	CAATTAGTCA	GCAACCATAG	TCCCGCCCCT	AACTCCGCCC	ATCCCGCCCC	TAACTCCGCC
2460	CAGTTCCGCC	CATTCTCCGC	CCCATGGCTG	ACTAATTTTT	TTTATTTATG	CAGAGGCCGA
2520	GGCCGCCTCG	GCCTCTGAGC	TATTCCAGAA	GTAGTGAGGA	GGCTTTTTTG	GAGGCCTAGG
2580	CTTTTGCAAA	GATCGATCAA	GAGACAGGAT	GAGGATCGTT	TCGCATGATT	GAACAAGATG
2640			GCCGCTTGGG	•		
2700	AACAGACAAT			TGTTCCGGCT		GGGCGCCCGG
2760			CTGTCCGGTG		•	
2820			ACGGGCGTTC			
2880			CTATTGGGCG	•		
2940			GTATCCATCA	:		
3000						
3060			TTCGACCACC			, ,
3120		·	GTCGATCAGG		•	
3180	CGCCAGCCGA	ACTGTTCGCC	AGGCTCAAGG	CGAGCATGCC	CGACGGCGAG	GATCTCGTCG

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16/56 FIG. T. (CONTINUED)

•	TCACCCATCC	CCATCCCTCC	TTGCCGAATA	TCATGGTGGA	AAATGGCCGC	· ምጥጥጥርጥርርልጥ
3240						
3300	TCATCGACTG	TGGCCGGCTG	GGTGTGGCGG	ACCGCTATCA	GGACATAGCG	TTGGCTACCC
3360	GTGATATTGC	TGAAGAGCTT	GGCGGCGAAT	GGGCTGACCG	CTTCCTCGTG	CTTTACGGTA
3420	TCGCCGCTCC	CGATTCGCAG	CGCATCGCCT	TCTATCGCCT	TCTTGACGAG	TTCTTCTGAG
3480	CGGGACTCTG	GGGTTCGAAA	TGACCGACCA	AGCGACGCCC	AACCTGCCAT	CACGAGATTT
3540	CGATTCCACC	GCCGCCTTCT	ATGAAAGGTT	GGGCTTCGGA	ATCGTTTTCC	GGGACGCCGG
3600	CTGGATGATC	CTCCAGCGCG	GGGATCTCAT	GCTGGAGTTC	TTCGCCCACC	CTAGGGGGAG
	GCTAACTGAA	ACACGGAAGG	AGACAATACC	GGAAGGAACC	CGCGCTATGA	CGGCAATAAA
3660	AAGACAGAAT	AAAACGCACG	GTGTTGGGTC	GTTTGTTCAT	AAACGCGGGG	TTCGGTCCCA
3720	GGGCTGGCAC	TCTGTCGATA	CCCCACCGAG	ACCCCATTGG	GGCCAATACG	CCCGCGTTTC
3780	TTCCTTTTCC	CCACCCCACC	CCCCAAGTTC	GGGTGAAGGC	CCAGGGCTCG	CAGCCAACGT
3840	CGGGGCGCA	GGCCCTGCCA	TAGCCTCAGG	TTACTCATAT	ATACTTTAGA	ТТСАТТТАВА
3900	er en		GGATCTAGGT		•	
3960	•					
4020			CGTTCCACTG			
4080	ATCTTCTTGA	GATCCTTTTT	TTCTGCGCGT	AATCTGCTGC	TTGCAAACAA	AAAAACCACC
4140	GCTACCAGCG	GTGGTTTGTT	TGCCGGATCA	AGAGCTACCA	ACTCTTTTTC	CGAAGGTAAC
4200	TGGCTTCAGC	AGAGCGCAGA	TACCAAATAC	TGTCCTTCTA	GTGTAGCCGT	AGTTAGGCCA
4260	CCACTTCAAG	AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCAGT
4320	GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG	GACTCAAGAC	GATAGTTACC
4380	GGATAAGGCG	CAGCGGTCGG	GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	GCTTGGAGCG
	AACGACCTAC	ACCGAACTGA	GATACCTACA	GCGTGAGCTA	TGAGAAAGCG	CCACGCTTCC
4440	CGAAGGGAGA	AAGGCGGACA	GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC
4500	GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	TCTTTATAGT	CCTGTCGGGT	TTCGCCACCT
4560	CTGACTTGAG	CGTCGATTTT	TGTGATGCTC	GTCAGGGGG	CGGAGCCTAT	GGAAAAACGC
4620			GGTTCCTGGC			
4680						nonigitali
4729		ICCCCIGATÍ	CTGTGGATAA	CCGIAITACC	GCCATGCAT	
				• *		



18/56 F/G. 9.

				•		
SQ	SEQUENCE	5619 BP				
6 0	GATCCCCATG	AACCGTGCTT	TTAGCAGGAA	GAAAGACAAA	ACATGGATGC	ATACACCTGA
120	AGCTTTATCA	AAACATTTCA	TTCCCTATAA	TGCAAAGTTT	CTTGGCAGTA	CAGAAGTGGA
	ACAGCCAAAA	GGAACAGAAG	TTGTGAGAGA	TGCTGTAAGG	AAACTAAAGT	TTGCAAGACA
180	TATCAAGAAA	TCTGAAGGCC	AGAAAATTCC	TAAAGTGGAG	TTGCAAATAT	CAATTTATGG
240	AGTAAAAATT	CTAGAACCCA	AAACAAAGGA	AGTTCAACAC	AATTGCCAGC	TTCATAGAAT
300	ATCTTTTTGT	GCAGATGATA	AAACTGACAA	GAGGATATTC	ACTTTCATAT	GCAAAGATTC
360	TGAGTCAAAT	AAACATTTGT	GCTATGTATT	TGACAGCGAA	AAGTGTGCTG	AAGAGATCAC
420	TTTAACAATT	GGCCAAGCAT	TTGACCTGGC	ATACACGAAA	TTTCTAGAAT	CAGGAGGAAA
480	AGATGTTGAA	ACAAGAAAAC	AGATCGCAGG	GTTACAAAAA	AGAATCCAAG	ACTTAGAAAC
540			•		AACCAACTGA	
600				•	CCCTCCACTG	
660			•	•	CCTACTCGCA	
720					GACCTGTTTG	
780					GATATTCAAT	•
840						
900					GGCACAGTAT	
960					GGATCCATCG	
1020					CTGGTCGAGC	
1080					GGCGATGCCA	
1140	GCTGACCCTG	AAGTTCATCT	GCACCACCGG	CAAGCTGCCC	GTGCCCTGGC	CCACCCTCGT
1200	GACCACCCTG	ACCTACGGCG	TGCAGTGCTT	CAGCCGCTAC	CCCGACCACA	TGAAGCAGCA
1260	CGACTTCTTC	AAGTCCGCCA	TGCCCGAAGG	CTACGTCCAG	GAGCGCACCA	TCTTCTTCAA
1320	GGACGACGGC	AACTACAAGA	CCCGCGCCGA	GGTGAAGTTC	GAGGGCGACA	CCCTGGTGAA
1380	CCGCATCGAG	CTGAAGGGCA	TCGACTTCAA	GGAGGACGGC	AACATCCTGG	GGCACAAGCT
1440	GGAGTACAAC	TACAACAGCC	ACAACGTCTA	TATCATGGCC	GACAAGCAGA	AGAACGGCAT
1500	CAAGGTGAAC	TTCAAGATCC	GCCACAACAT	CGAGGACGGC	AGCGTGCAGC	TCGCCGACCA

19/56 FIG. 9. (CONTINUED)

1560		AACACCCCA	TCGGCGACGG	CCCCGTGCTG	CTGCCCGACA	ACCACTACCT
	GAGCACCCAG	TCCGCCCTGA	GCAAAGACCC	CAACGAGAAG	CGCGATCACA	TGGTCCTGCT
1620	GGAGTTCGTG	ACCGCCGCCG	GGATCACTCT	CGGCATGGAC	GAGCTGTACA	AGTAAAGCGG
1680		AGATCATAAT	CAGCCATACC	ACATTTGTAG	AGGTTTTACT	TGCTTTAAAA
1740	- ^/ ·	ACCTCCCCCT	GAACCTGAAA	CATAAAATGA	ATGCAATTGT	TGTTGTTAAC
1800		CAGCTTATAA	ТССТТАСААА	ТАААССААТА	GCATCACAAA	ТТТСАСАААТ
1860		TTTCACTGCA		•		
1920	•					
1980	GGCGTAAATT	GTAAGCGTTA	ATATTTTGTT	AAAATTCGCG	TTAAATTTTT	GTTAAATCAG
2040	•	AACCAATAGG	CCGAAATCGG	CAAAATCCCT	TATAAATCAA	AAGAATAGAC
2100	CGAGATAGGG	TTGAGTGTTG	TTCCAGTTTG	GAACAAGAGT	CCACTATTAA	AGAACGTGGA
2160	CTCCAACGTC	AAAGGGCGAA	AAACCGTCTA	TCAGGGCGAT	GGCCCACTAC	GTGAACCATC
2220	ACCCTAATCA	AGTTTTTTGG	GGTCGAGGTG	CCGTAAAGCA	CTAAATCGGA	ACCCTAAAGG
	GAGCCCCCGA	TTTAGAGCTT	GACGGGGAAA	GCCGGCGAAC	GTGGCGAGAA	AGGAAGGGAA
2280	GAAAGCGAAA	GGAGCGGGCG	CTAGGGCGCT	GGCAAGTGTA	GCGGTCACGC	TGCGCGTAAC
2340	CACCACACCC	GCCGCGCTTA	ATGCGCCGCT	ACAGGGCGCG	TCAGGTGGCA	CTTTTCGGGG
2400	AAATGTGCGC	GGAACCCCTA	TTTGTTTATT	ТТТСТАААТА	CATTCAAATA	TGTATCCGCT
2460	CATGAGACAA	TAACCCTGAT	AAATGCTTCA	ATAATATTGA	AAAAGGAAGA	GTCCTGAGGC
2520		AGCTGTGGAA	••		·	
2580						·
2640		GTATGCAAAG	·	•		
2700	CCAGGCTCCC	CAGCAGGCAG	AAGTATGCAA	AGCATGCATC	TCAATTAGTC	AGCAACCATA
2760	GTCCCGCCCC	TAACTCCGCC	CATCCCGCCC	CTAACTCCGC	CCAGTTCCGC	CCATTCTCCG
2820	CCCCATGGCT	GACTAATTTT	TTTTATTTAT	GCAGAGGCCG	AGGCCGCCTC	GGCCTCTGAG
2880	CTATTCCAGA	AGTAGTGAGG	AGGCTTTTTT	GGAGGCCTAG	GCTTTTGCAA	AGATCGATCA
2940	AGAGACAGGA	TGAGGATCGT	TTCGCATGAT	TGAACAAGAT	GGATTGCACG	CAGGTTCTCC
• • •	GGCCGCTTGG	GTGGAGAGGC	TATTCGGCTA	TGACTGGGCA	CAACAGACAA	TCGGCTGCTC
3000	TGATGCCGCC	GTGTTCCGGC	TGTCAGCGCA	GGGGCGCCCG	GTTCTTTTTG	TCAAGACCGA
3060	CCTGTCCGGT	GCCCTGAATG	AACTGCAAGA	CGAGGCAGCG	CGGCTATCGT	GGCTGGCCAC
3120	GACGGGCGTT	CCTTGCGCAG	CTGTGCTCGA	CGTTGTCACT	GAAGCGGGAA	GGGACTGGCT
3180		+ +- +				·

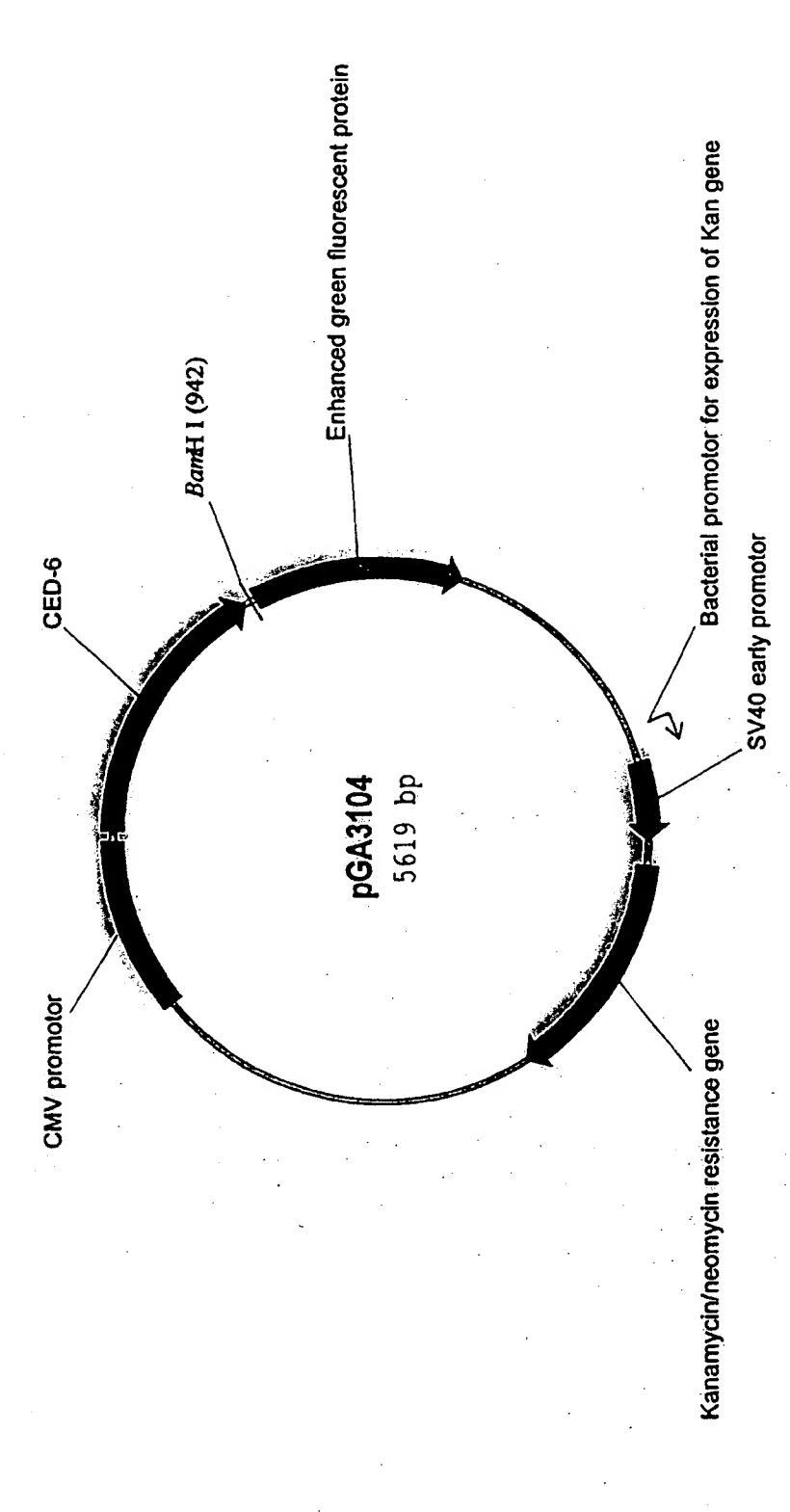
20/56 F/G. 9. (CONTINUED)

	2240	GCTATTGGGC	GAAGTGCCGG	GGCAGGATCT	CCTGTCATCT	CACCTTGCTC	CTGCCGAGAA
·	3240	AGTATCCATC	ATGGCTGATG	CAATGCGGCG	GCTGCATACG	CTTGATCCGG	CTACCTGCCC
	3300	ATTCGACCAC	CAAGCGAAAC	ATCGCATCGA	GCGAGCACGT	ACTCGGATGG	AAGCCGGTCT
	3360	TGTCGATCAG	GATGATCTGG	ACGAAGAGCA	TCAGGGGCTC	GCGCCAGCCG	AACTGTTCGC
	3420	CAGGCTCAAG	GCGAGCATGC	CCGACGGCGA	GGATCTCGTC	GTGACCCATG	GCGATGCCTG
·	3480	CTTGCCGAAT	ATCATGGTGG	AAAATGGCCG	CTTTTCTGGA	TTCATCGACT	GTGGCCGGCT
,	3540	GGGTGTGGCG	GACCGCTATC	AGGACATAGC	GTTGGCTACC	CGTGATATTG	CTGAAGAGCT
	3600	TGGCGGCGAA	TGGGCTGACC	GCTTCCTCGT	GCTTTACGGT	ATCGCCGCTC	CCGATTCGCA
	3660	GCGCATCGCC	TTCTATCGCC	TTCTTGACGA	GTTCTTCTGA	GCGGGACTCT	GGGGTTCGAA
•	3720	ATGACCGACC	AAGCGACGCC	CAACCTGCCA	TCACGAGATT	TCGATTCCAC	CGCCGCCTTC
	3780	TATGAAAGGT	TGGGCTTCGG	AATCGTTTTC	CGGGACGCCG	GCTGGATGAT	CCTCCAGCGC
	3840	GGGGATCTCA	TGCTGGAGTT	CTTCGCCCAC	CCTAGGGGGA	GGCTAACTGA	AACACGGAAG
·	3900	GAGACAATAC	CGGAAGGAAC	CCGCGCTATG	ACGGCAATAA	AAAGACAGAA	TAAAACGCAC
	3960	GGTGTTGGGT	CGTTTGTTCA	TAAACGCGGG	GTTCGGTCCC	AGGGCTGGCA	CTCTGTCGAT
	4020	ACCCCACCGA	GACCCCATTG	GGGCCAATAC	GCCCGCGTTT	CTTCCTTTTC	CCCACCCCAC
	4080	CCCCCAAGTT	CGGGTGAAGG	CCCAGGGCTC	GCAGCCAACG	TCGGGGCGGC	AGGCCCTGCC
	4140	ATAGCCTCAG	GTTACTCATA	TATACTTTAG	ATTGATTTAA	AACTTCATTT	TTAATTTAAA
•	4200	AGGATCTAGG	TGAAGATCCT	TTTTGATAAT	CTCATGACCA	AAATCCCTTA	ACGTGAGTTT
•	4260	TCGTTCCACT	GAGCGTCAGA	CCCCGTAGAA	AAGATCAAAG	GATCTTCTTG	AGATCCTTTT
	4320	TTTCTGCGCG	TAATCTGCTG	CTTGCAAACA	AAAAAACCAC	CGCTACCAGC	GGTGGTTTGT
	4380	TTGCCGGATC	AAGAGCTACC	AACTCTTTTT	CCGAAGGTAA	CTGGCTTCAG	CAGAGCGCAG
	4440	ATACCAAATA	CTGTCCTTCT	AGTGTAGCCG	TAGTTAGGCC	ACCACTTCAA	GAACTCTGTA
	4500	GCACCGCCTA	CATACCTCGC	TCTGCTAATC	CTGTTACCAG	TGGCTGCTGC	CAGTGGCGAT
	4560	AAGTCGTGTC	TTACCGGGTT	GGACTCAAGA	CGATAGTTAC	CGGATAAGGC	GCAGCGGTCG
	4620	GGCTGAACGG	GGGGTTCGTG	CACACAGCCC	AGCTTGGAGC	GAACGACCTA	CACCGAACTG
	4680	AGATACCTAC	AGCGTGAGCT	ATGAGAAAGC	GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC
	4740	AGGTATCCGG	TAAGCGGCAG	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	TCCAGGGGGA
	4800	AACGCCTGGT	ATCTTTATAG	TCCTGTCGGG	TTTCGCCACC	TCTGACTTGA	GCGTCGATTT
	4860						•

FIG. 9. (CONTINUED)

TTGTGATGCT CGTCAGGGGG GCGGAGCCTA TGGAAAAACG CCAGCAACGC GGCCTTTTTA

4920			00000001	100.1111.00	00.100.21000	0000111111
	CGGTTCCTGG	CCTTTTGCTG	GCCTTTTGCT	CACATGTTCT	TTCCTGCGTT	ATCCCCTGAT
4980						
5040	TCTGTGGATA	ACCGTATTAC	CGCCATGCAT	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC
2040	ATTAGTTCAT	AGCCCATATA	TGGAGTTCCG	CGTTACATAA	CTTACGGTAA	ATGGCCCGCC
5100					·	,
5160	TGGCTGACCG	CCCAACGACC	CCCGCCCATT	GACGTCAATA	ATGACGTATG	TTCCCATAGT
5160	AACGCCAATA	GGGACTTTCC	ATTGACGTCA	ATGGGTGGAG	TATTTACGGT	AAACTGCCCA
5220						
5000	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC	AAGTACGCCC	CCTATTGACG	TCAATGACGG
5280	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA	CATGACCTTA	TGGGACTTTC	CTACTTGGCA
5340				0.1.10.1001111		
	GTACATCTAC	GTATTAGTCA	TCGCTATTAC	CATGGTGATG	CGGTTTTGGC	AGTACATCAA
5400	TOCOCOTOCA	TAGCGGTTTG	カクサクカククク	እ ጥ ጥጥር ለአለርጥ	CTCCACCCCA	መመ <i>ር አ ርር</i> ጥር እ አ
5460	IGGGCGIGGA	INGCGGTITG	ACTCACGGGG	ATTICCAAGT	CICCACCCCA	TIGACGICAA
	TGGGAGTTTG	TTTTGGCACC	AAAATCAACG	GGACTTTCCA	AAATGTCGTA	ACAACTCCGC
5520				> 0000000000	C. C	
5580	CCCATTGACG	CAAATGGGCG	GTAGGCGTGT	ACGGTGGGAG	GTCTATATAA	GCAGAGCTGG
	TTTAGTGAAC	CGTCAGATCC	GCTAGCGCTA	CCGGACTCA		
5619					-	· · · · · · · · · · · · · · · · · · ·
<i>()</i>					•	



16.10

FIG. 11. 23/56

pcDNA3.1/His/LacZ circular DNA; 8578 BP ID SEQUENCE 8578 BP; SQ GACGGATCGG GAGATCTCCC GATCCCCTAT GGTCGACTCT CAGTACAATC TGCTCTGATG 60 CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG 120 CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC 180 TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT 240 GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA 300 TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC 360 CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC 420 ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACTGCCCA CTTGGCAGTA CATCAAGTGT 480 ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT 540 ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA 600 TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG 660 ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC 720 AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG 780 GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA 840 CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC 900 GTTTAAACTT AAGCTTACCA TGGGGGGTTC TCATCATCAT CATCATCATG GTATGGCTAG 960 CATGACTGGT GGACAGCAAA TGGGTCGGGA TCTGTACGAC GATGACGATA AGGTACCTAA 1020 GGATCAGCTT GGAGTTGATC CCGTCGTTTT ACAACGTCGT GACTGGGAAA ACCCTGGCGT 1080 TACCCAACTT AATCGCCTTG CAGCACATCC CCCTTTCGCC AGCTGGCGTA ATAGCGAAGA 1140 GGCCCGCACC GATCGCCCTT CCCAACAGTT GCGCAGCCTG AATGGCGAAT GGCGCTTTGC 1200 CTGGTTTCCG GCACCAGAAG CGGTGCCGGA AAGCTGGCTG GAGTGCGATC TTCCTGAGGC 1260 CGATACTGTC GTCGTCCCCT CAAACTGGCA GATGCACGGT TACGATGCGC CCATCTACAC 1320 CAACGTAACC TATCCCATTA CGGTCAATCC GCCGTTTGTT CCCACGGAGA ATCCGACGGG 1380 TTGTTACTCG CTCACATTTA ATGTTGATGA AAGCTGGCTA CAGGAAGGCC AGACGCGAAT 1440 TATTTTTGAT GGCGTTAACT CGGCGTTTCA TCTGTGGTGC AACGGGCGCT GGGTCGGTTA 1500 CGGCCAGGAC AGTCGTTTGC CGTCTGAATT TGACCTGAGC GCATTTTTAC GCGCCGGAGA 1560 AAACCGCCTC GCGGTGATGG TGCTGCGTTG GAGTGACGGC AGTTATCTGG AAGATCAGGA 1620 TATGTGGCGG ATGAGCGGCA TTTTCCGTGA CGTCTCGTTG CTGCATAAAC CGACTACACA 1680 AATCAGCGAT TTCCATGTTG CCACTCGCTT TAATGATGAT TTCAGCCGCG CTGTACTGGA 1740 1800 GGCTGAAGTT CAGATGTGCG GCGAGTTGCG TGACTACCTA CGGGTAACAG TTTCTTTATG GCAGGGTGAA ACGCAGGTCG CCAGCGGCAC CGCGCCTTTC GGCGGTGAAA TTATCGATGA 1860 GCGTGGTGGT TATGCCGATC GCGTCACACT ACGTCTGAAC GTCGAAAAACC CGAAACTGTG 1920 GAGCGCCGAA ATCCCGAATC TCTATCGTGC GGTGGTTGAA CTGCACACCG CCGACGGCAC 1980 GCTGATTGAA GCAGAAGCCT GCGATGTCGG TTTCCGCGAG GTGCGGATTG AAAATGGTCT 2040 GCTGCTGCTG AACGGCAAGC CGTTGCTGAT TCGAGGCGTT AACCGTCACG AGCATCATCC 2100 TCTGCATGGT CAGGTCATGG ATGAGCAGAC GATGGTGCAG GATATCCTGC TGATGAAGCA 2160 GAACAACTTT AACGCCGTGC GCTGTTCGCA TTATCCGAAC CATCCGCTGT GGTACACGCT 2220 GTGCGACCGC TACGGCCTGT ATGTGGTGGA TGAAGCCAAT ATTGAAACCC ACGGCATGGT 2280 GCCAATGAAT CGTCTGACCG ATGATCCGCG CTGGCTACCG GCGATGAGCG AACGCGTAAC 2340 GCGAATGGTG CAGCGCGATC GTAATCACCC GAGTGTGATC ATCTGGTCGC TGGGGAATGA 2400 ATCAGGCCAC GGCGCTARTC ACGACGCGCT GTATCGCTGG ATCAAATCTG TCGATCCTTC 2460 CCGCCCGGTG CAGTATGAAG GCGGCGGAGC CGACACCACG GCCACCGATA TTATTTGCCC 2520 GATGTACGCG CGCGTGGATG AAGACCAGCC CTTCCCGGCT GTGCCGAAAT GGTCCATCAA 2580 AAAATGGCTT TCGCTACCTG GAGAGACGCG CCCGCTGATC CTTTGCGAAT ACGCCCACGC 2640 GATGGGTÄAC AGTCTTGGCG GTTTCGCTAA ATACTGGCAG GCGTTTCGTC AGTATCCCCG 2700 TTTACAGGGC GGCTTCGTCT GGGACTGGGT GGATCAGTCG CTGATTAAAT ATGATGAAAA 2760 CGGCAACCCG TGGTCGGCTT ACGGCGGTGA TTTTGGCGAT ACGCCGAACG ATCGCCAGTT 2820 2880 CTGTATGAAC GGTCTGGTCT TTGCCGACCG CACGCCGCAT CCAGCGCTGA CGGAAGCAAA ACACCAGCAG CAGTTTTTCC AGTTCCGTTT ATCCGGGCAA ACCATCGAAG TGACCAGCGA 2940 ATACCTGTTC CGTCATAGCG ATAACGAGCT CCTGCACTGG ATGGTGGCGC TGGATGGTAA 3000 GCCGCTGGCA AGCGGTGAAG TGCCTCTGGA TGTCGCTCCA CAAGGTAAAC AGTTGATTGA 3060 ACTGCCTGAA CTACCGCAGC CGGAGAGCGC CGGGCAACTC TGGCTCACAG TACGCGTAGT 3120 3180 GCAACCGAAC GCGACCGTAT GGTCAGAAGC CGGGCACATC AGCGCCTGGC AGCAGTGGCG TCTGGCGGAA AACCTCAGTG TGACGCTCCC CGCCGCGTCC CACGCCATCC CGCATCTGAC 3240

24/56 F/G. H. (CONTINUED)

CACCAGCGAA ATGGATTTTT GCATCGAGCT GGGTAATAAG CGTTGGCAAT TTAACCGCCA 3300 GTCAGGCTTT CTTTCACAGA TGTGGATTGG CGATAAAAAA CAACTGCTGA CGCCGCTGCG 3360 3420 CGATCAGTTC ACCCGTGCAC CGCTGGATAA CGACATTGGC GTAAGTGAAG CGACCCGCAT TGACCCTAAC GCCTGGGTCG AACGCTGGAA GGCGGCGGGC CATTACCAGG CCGAAGCAGC 3480 GTTGTTGCAG TGCACGGCAG ATACACTTGC TGATGCGGTG CTGATTACGA CCGCTCACGC 3540 GTGGCAGCAT CAGGGGAAAA CCTTATTTAT CAGCCGGAAA ACCTACCGGA TTGATGGTAG 3600 TGGTCAAATG GCGATTACCG TTGATGTTGA AGTGGCGAGC GATACACCGC ATCCGGCGCG 3660 3720 GATTGGCCTG AACTGCCAGC TGGCGCAGGT AGCAGAGCGG GTAAACTGGC TCGGATTAGG GCCGCAAGAA AACTATCCCG ACCGCCTTAC TGCCGCCTGT TTTGACCGCT GGGATCTGCC 3780 ATTGTCAGAC ATGTATACCC CGTACGTCTT CCCGAGCGAA AACGGTCTGC GCTGCGGGAC 3840 GCGCGAATTG AATTATGGCC CACACCAGTG GCGCGGCGAC TTCCAGTTCA ACATCAGCCG 3900 CTACAGTCAA CAGCAACTGA TGGAAACCAG CCATCGCCAT CTGCTGCACG CGGAAGAAGG 3960 CACATGGCTG AATATCGACG GTTTCCATAT GGGGATTGGT GGCGACGACT CCTGGAGCCC 4020 GTCAGTATCG GCGGAGTTCC AGCTGAGCGC CGGTCGCTAC CATTACCAGT TGGTCTGGTG 4080 TCAAAAATAA TAAAGCCGAA TTCTGCAGAT ATCCAGCACA GTGGCGGCCG CTCGAGTCTA 4140 4200 GAGGGCCCGT TTAAACCCGC TGATCAGCCT CGACTGTGCC TTCTAGTTGC CAGCCATCTG TTGTTTGCCC CTCCCCGTG CCTTCCTTGA CCCTGGAAGG TGCCACTCCC ACTGTCCTTT 4260 4320 CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG GTGTCATTCT ATTCTGGGGG 4380 GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGCT TCTGAGGCGG AAAGAACCAG CTGGGGCTCT AGGGGGTATC 4440 CCCACGCGCC CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA 4500 CCGCTACACT TGCCAGCGCC CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG 4560 4620 CCACGTTCGC CGGCTTTCCC CGTCAAGCTC TAAATCGGGG CATCCCTTTA GGGTTCCGAT TTAGTGCTTT ACGGCACCTC GACCCCAAAA AACTTGATTA GGGTGATGGT TCACGTAGTG 4680 GGCCATCGCC CTGATAGACG GTTTTTCGCC CTTTGACGTT GGAGTCCACG TTCTTTAATA 4740 GTGGACTCTT GTTCCAAACT GGAACAACAC TCAACCCTAT CTCGGTCTAT TCTTTTGATT 4800 TATAAGGGAT TTTGGGGATT TCGGCCTATT GGTTAAAAAA TGAGCTGATT TAACAAAAAT 4860 TTAACGCGAA TTAATTCTGT GGAATGTGTG TCAGTTAGGG TGTGGAAAGT CCCCAGGCTC 4920 4980 CCCAGGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA GTCAGCAACC AGGTGTGGAA AGTCCCCAGG CTCCCCAGCA GGCAGAAGTA TGCAAAGCAT GCATCTCAAT TAGTCAGCAA 5040 5100 CCATAGTCCC GCCCCTAACT CCGCCCATCC CGCCCCTAAC TCCGCCCAGT TCCGCCCATT 5160 CTCCGCCCCA TGGCTGACTA ATTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCTGCCT CTGAGCTATT CCAGAAGTAG TGAGGAGGCT TTTTTGGAGG CCTAGGCTTT TGCAAAAAGC 5220 5280 TCCCGGGAGC TTGTATATCC ATTTTCGGAT CTGATCAAGA GACAGGATGA GGATCGTTTC 5340 GCATGATTGA ACAAGATGGA TTGCACGCAG GTTCTCCGGC CGCTTGGGTG GAGAGGCTAT 5400 TCGGCTATGA CTGGGCACAA CAGACAATCG GCTGCTCTGA TGCCGCCGTG TTCCGGCTGT CAGCGCAGGG GCGCCCGGTT CTTTTTGTCA AGACCGACCT GTCCGGTGCC CTGAATGAAC 5460 TGCAGGACGA GGCAGCGGG CTATCGTGGC TGGCCACGAC GGGCGTTCCT TGCGCAGCTG 5520 5580 TGCTCGACGT TGTCACTGAA GCGGGAAGGG ACTGGCTGCT ATTGGGCGAA GTGCCGGGGC 5640 AGGATCTCCT GTCATCTCAC CTTGCTCCTG CCGAGAAAGT ATCCATCATG GCTGATGCAA TGCGGCGGCT GCATACGCTT GATCCGGCTA CCTGCCCATT CGACCACCAA GCGAAACATC 5700 -5760 GCATCGAGCG AGCACGTACT CGGATGGAAG CCGGTCTTGT CGATCAGGAT GATCTGGACG AAGAGCATCA GGGGCTCGCG CCAGCCGAAC TGTTCGCCAG GCTCAAGGCG CGCATGCCCG 5820 5880 ACGCCGAGGA TCTCGTCGTG ACCCATGGCG ATGCCTGCTT GCCGAATATC ATGGTGGAAA 5940 ATGCCGCTT TTCTGGATTC ATCGACTGTG GCCGGCTGGG TGTGGCGGAC CGCTATCAGG 6000 ACATAGCGTT GGCTACCCGT GATATTGCTG AAGAGCTTGG CGGCGAATGG GCTGACCGCT 6060 TCCTCGTGCT TTACGGTATC GCCGCTCCCG ATTCGCAGCG CATCGCCTTC TATCGCCTTC TTGACGAGTT CTTCTGAGCG GGACTCTGGG GTTCGAAATG ACCGACCAAG CGACGCCCAA 6120 CCTGCCATCA CGAGATTTCG ATTCCACCGC CGCCTTCTAT GAAAGGTTGG GCTTCGGAAT 6180 CGTTTTCCGG GACGCCGGCT GGATGATCCT CCAGCGCGGG GATCTCATGC TGGAGTTCTT 6240 6300 CGCCCACCCC AACTTGTTTA TTGCAGCTTA TAATGGTTAC AAATAAAGCA ATAGCATCAC AAATTTCACA AATAAAGCAT TTTTTTCACT GCATTCTAGT TGTGGTTTGT CCAAACTCAT 6360 CAATGTATCT TATCATGTCT GTATACCGTC GACCTCTAGC TAGAGCTTGG CGTAATCATG 6420 GTCATAGCTG TTTCCTGTGT GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC 6480 CGGAAGCATA AAGTGTAAAG CCTGGGGTGC CTAATGAGTG AGCTAACTCA CATTAATTGC 6540 GTTGCGCTCA CTGCCCGCTT TCCAGTCGGG AAACCTGTCG TGCCAGCTGC ATTAATGAAT 6600 CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT CCTCGCTCAC 6660

FIG. 11. (CONTINUED)

	•	,					•
	TGACTCGCTG	CGCTCGGTCG	TTCGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	6720
	AATACGGTTA	TCCACAGAAT	CAGGGGATAA	. CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	6780
	GCAAAAGGCC	AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	6840
	CCCTGACGAG	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	6900
	ATAAAGATAC	CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	6960
	GCCGCTTACC	GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	AGCGTGGCGC	TTTCTCAATG	7020
	CTCACGCTGT	AGGTATCTCA	GTTCGGTGTA	GGTCGTTCGC	TCCAAGCTGG	GCTGTGTGCA	7080
	CGAACCCCCC	GTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	AACTATCGTC	TTGAGTCCAA	7140
	CCCGGTAAGA	CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	7200
	GAGGTATGTA	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	7260
	AAGGACÁGTA	TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	7320
	TAGCTCTTGA	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	7380
	GCAGATTACG	CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	7440
	TGACGCTCAG	TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG	7500
	GATCTTCACC	TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	7560
~	TGAGTAAACT	TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	7620
•	CTGTCTATTT	CGTTCATCCA	TAGTTGCCTG	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	7680
	GGAGGGCTTA	CCATCTGGCC	CCAGTGCTGC	AATGATACCG	CGAGACCCAC	GCTCACCGGC	7740
	TCCAGATTTA	TCAGCAATAA	ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA	GTGGTCCTGC.	7800
	AACTTTATCC	GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	GAAGCTAGAG	TAAGTAGTTC	7860
	GCCAGTTAAT	AGTTTGCGCA	ACGTTGTTGC	CATTGCTACA	GGCATCGTGG	TGTCACGCTC	7920
	GTCGTTTGGT	ATGGCTTCAT	TCAGCTCCGG	TTCCCAACGA	TCAAGGCGAG	TTACATGATC	7980
	CCCCATGTTG	TGCAAAAAAG	CGGTTAGCTC	CTTCGGTCCT	CCGATCGTTG	TCAGAAGTAA	8040
	GTTGGCCGCA	GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC	TTACTGTCAT	8100
	GCCATCCGTA	AGATGCTTTT	CTGTGACTGG	TGAGTACTCA	ACCAAGTCAT	TCTGAGAATA	8160
٠.	GTGTATGCGG	CGACCGAGTT	GCTCTTGCCC	GGCGTCAATA	CGGGATAATA	CCGCGCCACA	8220
	TAGCAGAACT	TTAAAAGTGC	TCATCATTGG	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	8280
-	GATCTTACCG	CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	CGTGCACCCA	ACTGATCTTC	8340
	AGCATCTTTT	ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	AAAATGCCGC	8400
	AAAAAAGGGA	ATAAGGGCGA	CACGGAAATG	TTGAATACTC	ATACTCTTCC	TTTTTCAATA	8460
	TTATTGAAGC	ATTTATCAGG	GTTATTGTCT	CATGAGCGGA	TACATATTTG	AATGTATTTA	8520
•	GAAAATAAA	CAAATAGGGG	TTCCGCGCAC	ATTTCCCCGA	AAAGTGCCAC	CTGACGTC	8578
	7.00	•		•			•

26/56 F/G. 12.

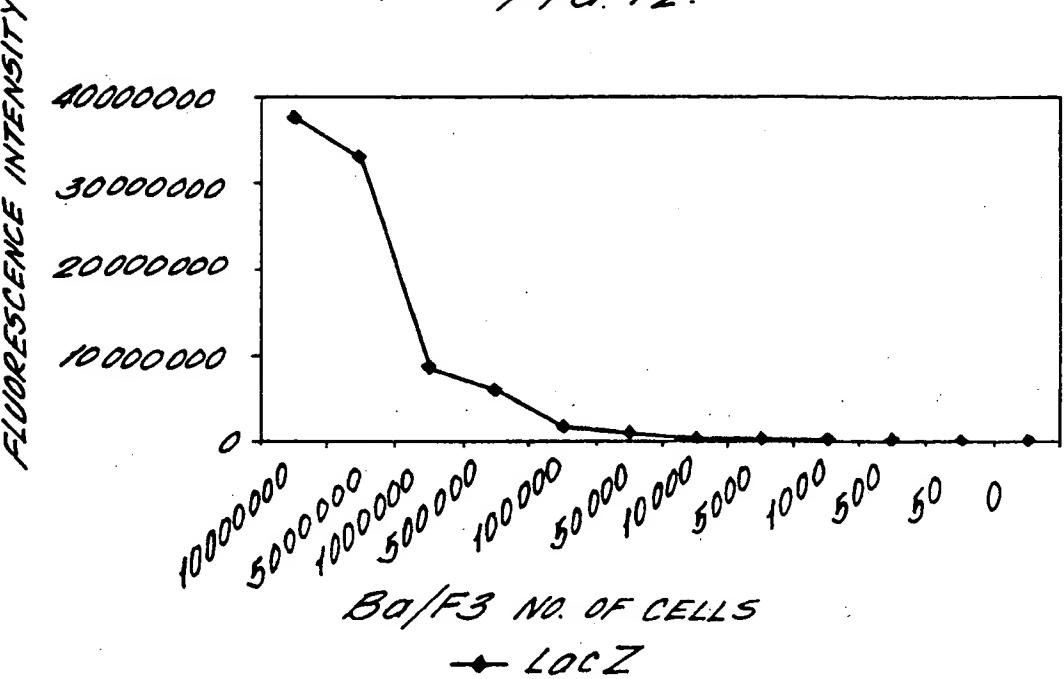
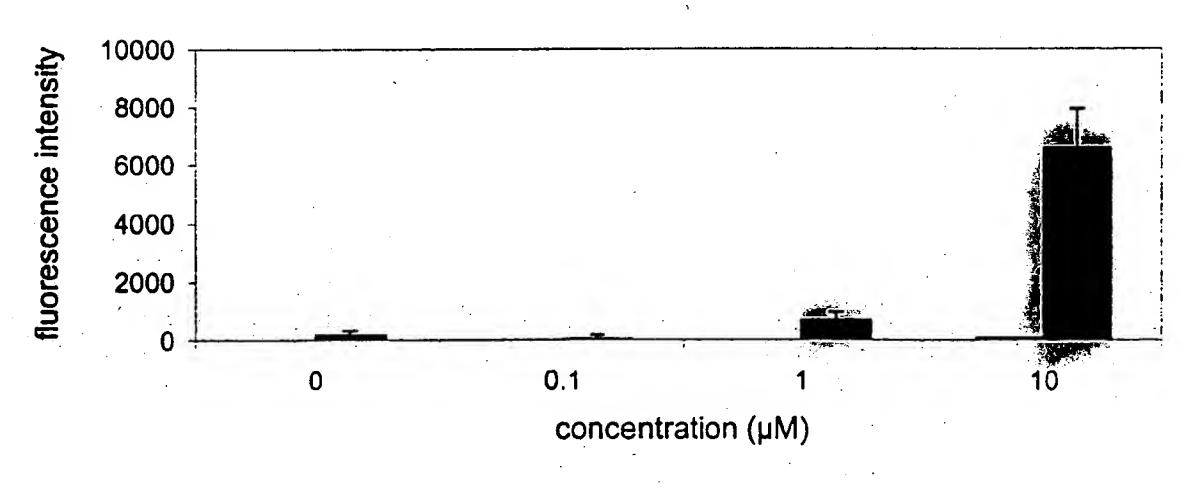
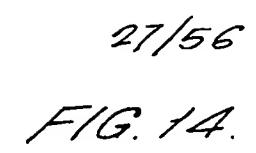
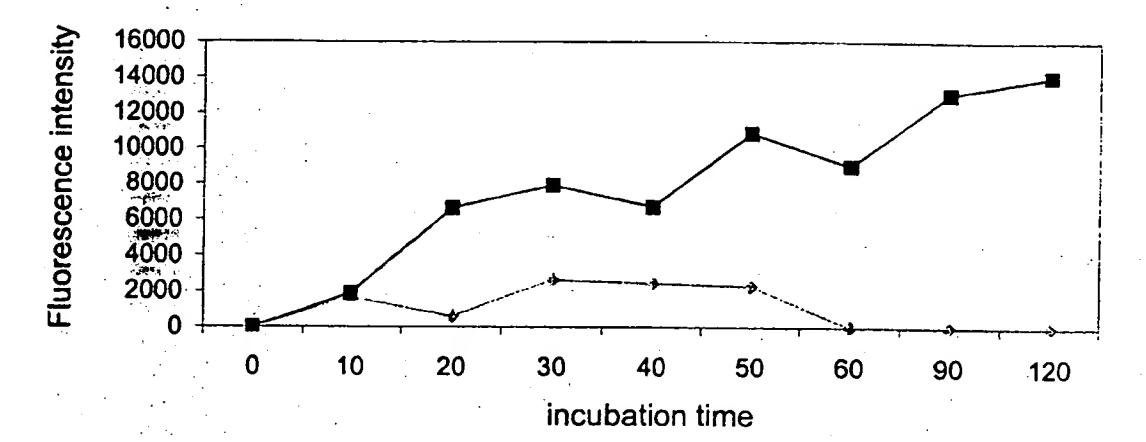


FIG. 13.



☐ Life Ba/F3 ■ Apoptotic Ba/F3





→ Life Ba/F3 → Apoptotic Ba/F3

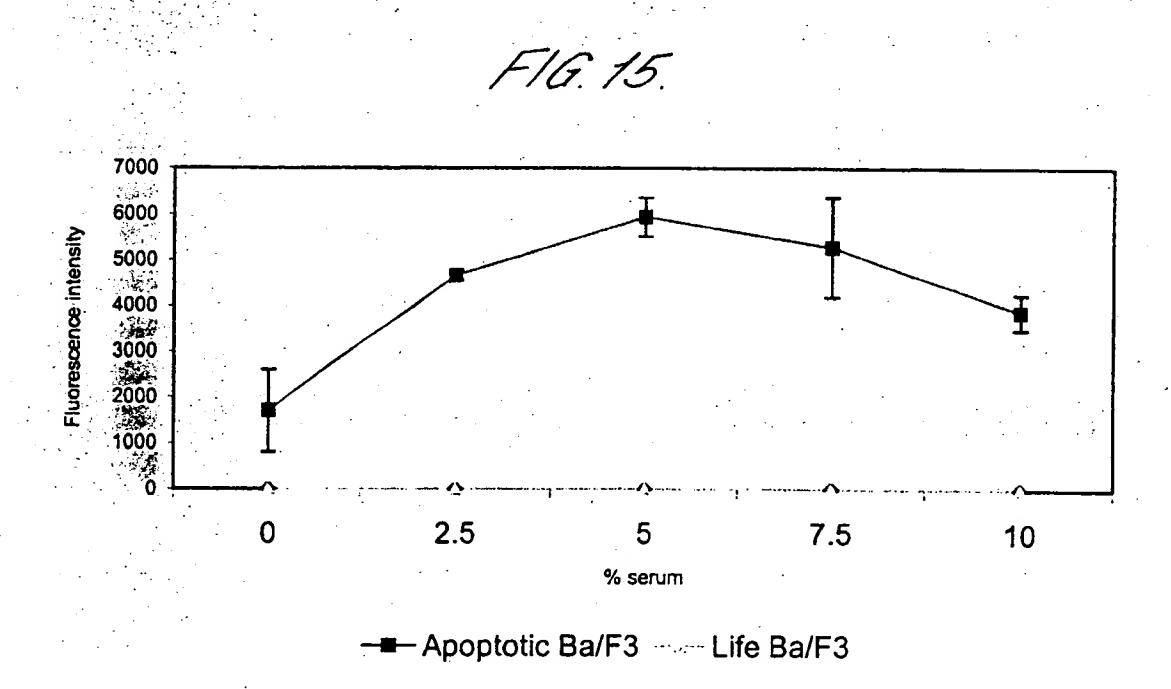


FIG. 16.

mnrafsrkkdktwmhtpealskhfipynakflgsteveqpkgtevvrdavrklkfarhikksegqkipk velqisiygvkilepktkevqhncqlhrisfcaddktdkriftfickdsesnkhlcyvfdsekcaeeitltigq afdlaytkflesggkdvetrkqiaglqkriqdletenmelknkvqdlenqlritqvsappagsmtpkspst difdmipfspishqssmptrngtqpppvpsrsteikrdlfgaepfdpfncgaadfppdiqskldemqegf kmgltlegtvfcldpldsrc

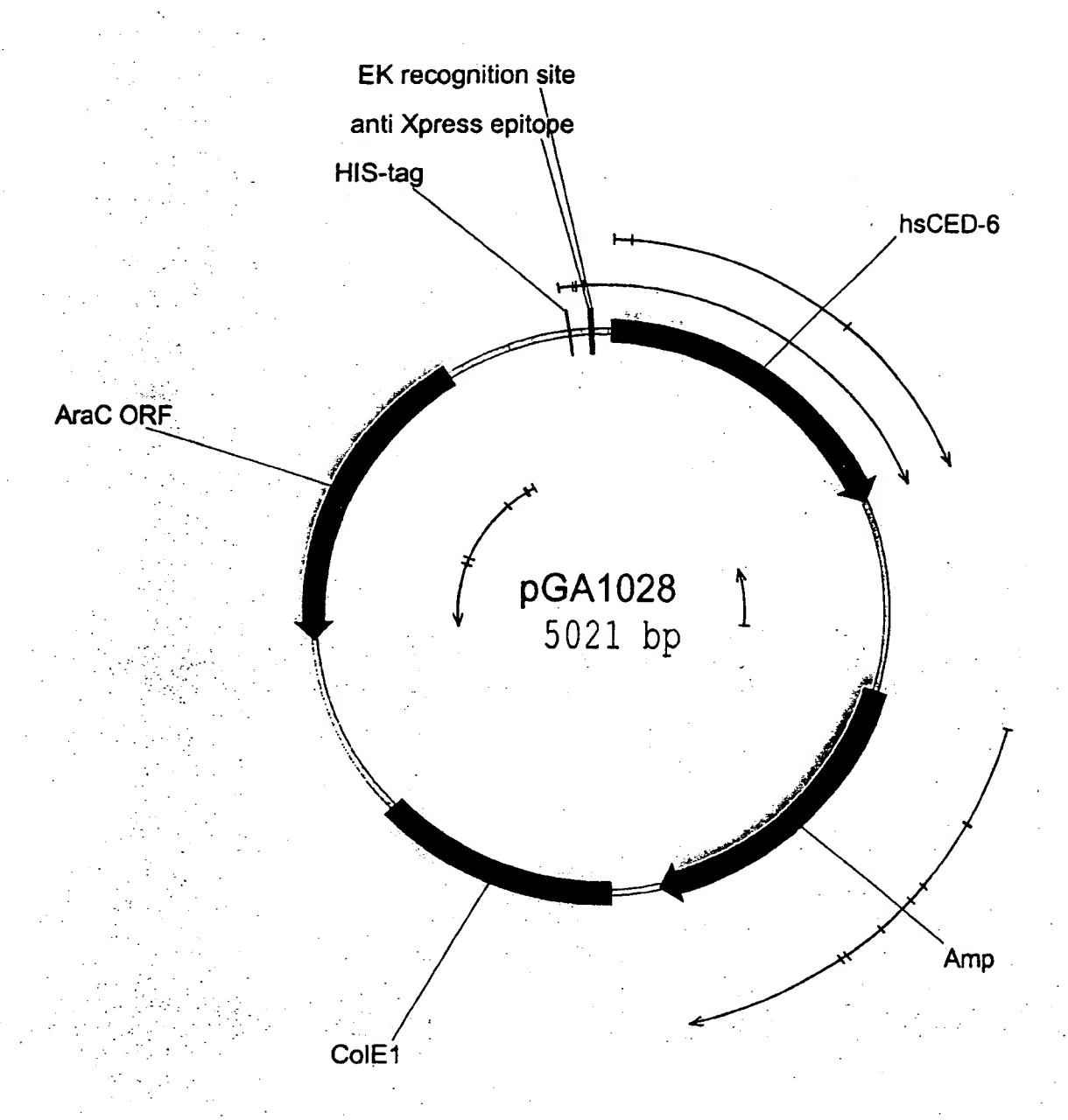
FIG. 17. 29/56

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pGA1028
ID
                                     circular DNA; 5021 BP
DE
     hCed-6cds in pBAD HisA
CC
     http://www.informaxinc.com/
CÇ
     pGA1028 in Top 10:
CC
     VNTAUTHORNAME | Nina cromheecke |
FT
     CDS
                     8..919
FT
                     /vntifkey="4"
FT
                     /label=hsCED-6
FT
     CDS
                     4918..4935
                     /vntifkey="4"
FT
FT
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     misc feature
FT
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FT
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     rep origin
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                     /vntifkey="33"
FŢ
                     /label=ColE1
FT
     CDS
                     3682..4560
FT
                     /vntifkey="4"
FT
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SQ
     SEQUENCE
                5021 BP;
     GATCCCCATG AACCGTGCTT TTAGCAGGAA GAAAGACAAA ACATGGATGC ATACACCTGA
                                                                               60
     AGCTTTATCA AAACATTTCA TTCCCTATAA TGCAAAGTTT CTTGGCAGTA CAGAAGTGGA
                                                                              120
     ACAGCCAAAA GGAACAGAAG TTGTGAGAGA TGCTGTAAGG AAACTAAAGT TTGCAAGACA
                                                                              180
     TATCAAGAAA TCTGAAGGCC AGAAAATTCC TAAAGTGGAG TTGCAAATAT CAATTTATGG
                                                                              240
    AGTAAAATT CTAGAACCCA AAACAAAGGA AGTTCAACAC AATTGCCAGC TTCATAGAAT
                                                                              300
    ATCTTTTGT GCAGATGATA AAACTGACAA GAGGATATTC ACTTTCATAT GCAAAGATTC
                                                                              360
    TGAGTCAAAT AAACATTTGT GCTATGTATT TGACAGCGAA AAGTGTGCTG AAGAGATCAC
                                                                              420
    TTTAACAATT GGCCAAGCAT TTGACCTGGC ATACACGAAA TTTCTAGAAT CAGGAGGAAA
                                                                              480
    AGATGTTGAA ACAAGAAAAC AGATCGCAGG GTTACAAAAA AGAATCCAAG ACTTAGAAAC
                                                                              540
    AGAAAATATG GAACTTAAAA ATAAAGTACA AGATTTGGAA AACCAACTGA GAATAACTCA
                                                                              600
    AGTATCAGCA CCTCCAGCAG GCAGTATGAC ACCTAAGTCG CCCTCCACTG ACATCTTTGA
                                                                              660
    TATGATTCCA TTTTCTCCAA TATCACACCA GTCTTCGATG CCTACTCGCA ATGGCACACA
                                                                              720
    GCCACCTCCA GTACCTAGTA GATCTACTGA GATTAAACGG GACCTGTTTG GAGCAGAACC
                                                                              780
    TTTTGACCCA TTTAACTGTG GAGCAGCAGA TTTCCCTCCA GATATTCAAT CAAAATTAGA
                                                                              840
    TGAGATGCAG GAGGGGTTCA AAATGGGACT AACTCTTGAA GGCACAGTAT TTTGTCTCGA
                                                                              900
    CCCGTTAGAC AGTAGGTGCT GAGTCGACGG TACCATATGG GAATTCGAAG CTTGGCTGTT
                                                                              960
    TTGGCGGATG AGAGAGATT TTCAGCCTGA TACAGATTAA ATCAGAACGC AGAAGCGGTC
                                                                             1020
    TGATAAAACA GAATTTGCCT GGCGGCAGTA GCGCGGTGGT CCCACCTGAC CCCATGCCGA
                                                                             1080
    ACTCAGAAGT GAAACGCCGT AGCGCCGATG GTAGTGTGGG GTCTCCCCAT GCGAGAGTAG
                                                                             1140
    GGAACTGCCA GGCATCAAAT AAAACGAAAG GCTCAGTCGA AAGACTGGGC CTTTCGTTTT
                                                                             1200
    ATCTGTTGTT TGTCGGTGAA CGCTCTCCTG AGTAGGACAA ATCCGCCGGG AGCGGATTTG
                                                                            1260
    AACGTTGCGA AGCAACGGCC CGGAGGGTGG CGGGCAGGAC GCCCGCCATA AACTGCCAGG
                                                                             1320
    CATCAAATTA AGCAGAAGGC CATCCTGACG GATGGCCTTT TTGCGTTTCT ACAAACTCTT
                                                                             1380
    TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT
                                                                             1440
    AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTC CGTGTCGCCC
                                                                             1500
    TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC TCACCCAGAA ACGCTGGTGA
                                                                             1560
    AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA CTGGATCTCA
                                                                            1620
    ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT
                                                                            1680
    TTAAAGTTCT GCTATGTGGC GCGGTATTAT CCCGTGTTGA CGCCGGGCAA GAGCAACTCG
                                                                            1740
    GTCGCCGCAT ACACTATICT CAGAATGACT TGGTTGAGTA CTCACCAGTC ACAGAAAAGC
                                                                            1800
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30/56 F/G. 17. (CONTINUED)

	_						
	ATCTTACGGA	TGGCATGACA	GTAAGAGAAT	TATGCAGTGC	TGCCATAACC	ATGAGTGATA	1860
	ACACTGCGGC	CAACTTACTT	CTGACAACGA	TCGGAGGACC	GAAGGAGCTA	ACCGCTTTTT	1920
	TGCACAACAT	GGGGGATCAT	GTAACTCGCC	TTGATCGTTG	GGAACCGGAG	CTGAATGAAG	1980
	CCATACCAAA	CGACGAGCGT	GACACCACGA	TGCCTGTAGC	AATGGCAACA	ACGTTGCGCA	2040
	AACTATTAAC	TGGCGAACTA	CTTACTCTAG	CTTCCCGGCA	ACAATTAATA	GACTGGATGG	2100
	AGGCGGATAA	AGTTGCAGGA	CCACTTCTGC	GCTCGGCCCT	TCCGGCTGGC	TGGTTTATTG	2160
	CTGATAAATC	TGGAGCCGGT	GAGCGTGGGT	CTCGCGGTAT	CATTGCAGCA	CTGGGGCCAG	2220
	ATGGTAAGCC	CTCCCGTATC	GTAGTTATCT	ACACGACGGG	GAGTCAGGCA	ACTATGGATG	2280
	AACGAAATAG	ACAGATCGCT	GAGATAGGTG	CCTCACTGAT	TAAGCATTGG	TAACTGTCAG	2340
	ACCAAGTTTA	CTCATATATA	CTTTAGATTG	ATTTAAAACT	TCATTTTTAA	TTTAAAAGGA	2400
	TCTAGGTGAA	GATCCTTTTT	GATAATCTCA	TGACCAAAAT	CCCTTAACGT	GAGTTTTCGT	2460
	TCCACTGAGC	GTCAGACCCC	GTAGAAAAGA	TCAAAGGATC	TTCTTGAGAT	CCTTTTTTC	2520
	TGCGCGTAAT	CTGCTGCTTG	CAAACAAAAA	AACCACCGCT	ACCAGCGGTG	GTTTGTTTGC	2580
	CGGATCAAGA.	GCTACCAACT	CTTTTTCCGA	AGGTAACTGG	CTTCAGCAGA	GCGCAGATAC	2640
	CAAATACTGT	CCTTCTAGTG	TAGCCGTAGT	TAGGCCACCA	CTTCAAGAAC	TCTGTAGCAC	2700
	CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCAGTGGC	TGCTGCCAGT	GGCGATAAGT	2760
	CGTGTCTTAC	CGGGTTGGAC	TCAAGACGAT	AGTTACCGGA	TAAGGCGCAG	CGGTCGGGCT	2820
	GAACGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC	GACCTACACC	GAACTGAGAT	2880
	ACCTACAGCG	TGAGCTATGA	GAAAGCGCCA	CGCTTCCCGA	AGGGAGAAAG	GCGGACAGGT	2940
	ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG	GGAGCTTCCA	GGGGGAAACG	3000
	CCTGGTATCT	TTATAGTCCT	GTCGGGTTTC	GCCACCTCTG	ACTTGAGCGT	CGATTTTTGT	3060
	GATGCTCGTC	AGGGGGGGG	AGCCTATGGA	AAAACGCCAG	CAACGCGGCC	TTTTTACGGT	3120
	TCCTGGCCTT	TTGCTGGCCT	TTTGCTCACA	TGTTCTTTCC	TGCGTTATCC	CCTGATTCTG	3180
	TGGATAACCG	TATTACCGCC	-	CTGATACCGC	TCGCCGCAGC	CGAACGACCG	3240
	AGCGCAGCGA	GTCAGTGAGC	GAGGAAGCGG	•	GATGCGGTAT	TTTCTCCTTA	3300
	CGCATCTGTG	CGGTATTTCA		GGTGCACTCT		TGCTCTGATG	3360
	•	AAGCCAGTAT			* · ·		3420
	CCGACACCCG	CCAACACCCG		•	TGTCTGCTCC	CGGCATCCGC	3480
	TTACAGACAA	GCTGTGACCG	•	CTGCATGTGT		CACCGTCATC	3540
	_	GCGAGGCAGC	AGATCAATTC			ATGCATAATG	3600
		ATGGACGAAG		•		TCAAGCCGTC	3660
	AATTGTCTGA	•	ATTATGACAA	•			3720
		CGGAACTCGC	ı	•	TTTTTAAATA	•	3780
	ATAGAGTTGA	• •		•	GCGATAGGCA	TCCGGGTGGT	3840
		AGCTTCGCCT				AGACGCTAAT	3900
	CCCTAACTGC	TGGCGGAAAA		ACGCGACGGC		CATGCTGTGC	3960
		ATATCAAAAT	•	CAGGTGATCG	•	GACAAGCCTC	4020
	GCGTACCCGA	TTATCCATCG		• •	ATCGCTTCCA	TGCGCCGCAG	4080
	TAACAATTGC	TCAAGCAGAT	▼ - · · · · · · · · · · · · · · · · · ·	CAGCTCCGAA		CCCCTTGCCC	4140
				GAAATGCGGC		CATCCGGGCG	4200
				and the second of the second o	CATTCATGCC		4260
			GGTGATACCA				4320
			ACAGCAAAAT			·	4380
•		ACCACCCCT	***	•	AGAATATAAC		4440
	,		AATCGAGATA	•	·	. – –	4500
			AGTATCCCGG			•	4560
		CTCCCGCCAT	<u>-</u>	•	CCATATTGCA		4620
		GTCTTTTACT	•		CCGGTAACCC	•	4680
		TAACAAAGCG			ACGCGTAACA	-	4740
		AGAAAAGTCC			GTCACACTTT	-	4800
		TCCATAAGAT			TTTTTATCGC		4860
		TACCCGTTTT			TAACCATGGG		4920
	· -	ATCATGGTAT				TUGGGATUTG	4980
	TACGACGATG	ACGATAAGGA	TCGATGGGGA	I CCGAGC I CG	A		5021
		•					

31/56 F1G. 18.



32/56 FIG. 19.

PGL2control (promega)

1		TCTTACGCGT AGAATGCGCA		•	
51		GTCAGCAACC CAGTCGTTGG			
101		CGCCCAGTTC	•		
151	- ·	TATGCAGAGG ATACGTCTCC			
201		AGGAGGCTTT TCCTCCGAAA			
251		TACTGTTGGT ATGACAACCA			· -
301		CGGCGCCATT		•	
351		AAGGCTATGA TTCCGATACT			
401		TGCACATATC ACGTGTATAG			
451		TTCGGTTGGC AAGCCAACCG			
501.	AAATCACAGA TTTAGTGTCT	ATCGTCGTAT TAGCAGCATA		CTCTCTTCAA GAGAGAAGTT	TTCTTTATGC AAGAAATACG
551	•	CGCGTTATTT GCGCAATAAA			
601		AACGTGAATT TTGCACTTAA		-	
651		GTTTCCAAAA CAAAGGTTTT		AAAAATTTTG TTTTTAAAAC	
701		AATCATCÇAA TTAGTAGGTT	1		
751		TTCAGTCGAT AAGTCAGCTA			
801		GAATACGATT CTTATGCTAA		· · ·	
851		GATCATGAAC CTAGTACTTG			

33/56 F/G. 19. (CONTINUED)

901		CTCATAGAAC GAGTATCTTG		ATGCCAGAGA TACGGTCTCT
951		GGCAATCAAA CCGTTAGTTT		
1001		TCACGGTTTT AGTGCCAAAA		
1051		GAGTCGTCTT CTCAGCAGAA		
1101	* * *	CAGGATTACA GTCCTAATGT		
1151		CTTCGCCAAA GAAGCGGTTT		- -
1201		AAATTGCTTC TTTAACGAAG	_	AGGAAGTCGG TCCTTCAGCC
	GGAAGCGGTT CCTTCGCCAA			
1301	GGCTCACTGA CCGAGTGACT	•		GGGGGATGAT CCCCCTACTA
1351	AAACCGGGCG TTTGGCCCGC	CGGTCGGTAA GCCAGCCATT		_
1401	GGATCTGGAT CCTAGACCTA	ACCGGGAAAA TGGCCCTTTT		
1451	GTGTGAGAGG CACACTCTCC	TCCTATGATT AGGATACTAA		
1501	ACCAACGCCT TGGTTGCGGA	TGATTGACAA ACTAACTGTT		
1551	TTACTGGGAC AATGACCCTG	GAAGACGAAC CTTCTGCTTG		·
1601	TGATTAAGTA ACTAATTCAT	CAAAGGCTAT GTTTCCGATA		
1651	TTGCTCCAAC AACGAGGTTG	ACCCCAACAT TGGGGTTGTA	•	
1701		GGTGAACTTC CCACTTGAAG		
1751		GGAAAAAGAG CCTTTTTCTC		
1801	ACCGCGAAAA TGGCGCTTTT	AGTTGCGCGG TCAACGCGCC		

34/56 F/G. 19. (CONTINUED)

1851		GGAAAACTCG CCTTTTGAGC			
1901					TCGGGGCGGC AGCCCCGCCG
1951		GAGCAGACAT CTCGTCTGTA			TTGGACAAAC AACCTGTTTG
2001		ATGCAGTGAA TACGTCACTT			ATTTGTGATG TAAACACTAC
2051		ATTTGTAACC TAAACATTGG			
2101		TTCATTTTAT AAGTAAAATA			
2151	TTTTTAAAGC AAAAATTTCG	AAGTAAAACC TTCATTTTGG		TGGTAAAATC ACCATTTTAG	GATAAGGATC CTATTCCTAG
2201	_	AGCGGAGAAT TCGCCTCTTA			AGGGGCGGGA TCCCCGCCCT
2251		TAGGGGCGGG ATCCCCGCCC	-	•	
2301		TTCTGCCTGC AAGACGGACG	• •		•
2351		TTGAGATGCA AACTCTACGT		•	
2401		TCCACACCCT AGGTGTGGGA			
2451		CTTGAGAGCC GAACTCTCGG	•		
2501	•	CTATCGTCGC GATAGCAGCG	. •		
2551	ACTCGTAGGA TGAGCATCCT	CAGGTGCCGG GTCCACGGCC	· -		-
2601		CGGTCGTTCG GCCAGCAAGC			
2651		CGGTTATCCA GCCAATAGGT			
2701	TGTGAGCAAA ACACTCGTTT	AGGCCAGCAA TCCGGTCGTT			
2751	CTGGCGTTTT GACCGCAAAA	TCCATAGGCT AGGTATCCGA		_	

35/56 F1G. 19. (CONTINUED) ...

2801	•	CAGAGGTGGC GTCTCCACCG			
2851	- · ·	TGGAAGCTCC ACCTTCGAGG			
2901	CTTACCGGAT GAATGGCCTA	ACCTGTCCGC TGGACAGGCG			
2951	TCAATGCTCA AGTTACGAGT	CGCTGTAGGT GCGACATCCA			•
3001	AGCTGGGCTG TCGACCCGAC	TGTGCACGAA ACACGTGCTT			
3051		ATCGTCTTGA TAGCAGAACT		·	
3101	•	GCCACTGGTA CGGTGACCAT			
3151		GTTCTTGAAG CAAGAACTTC			
	ACAGTATTTG TGTCATAAAC	•		•	•
	AGTTGGTAGC TCAACCATCG			•	
•	TTTTTGTTTG AAAAACAAAC				
3351	GATCCTTTGA CTAGGAAACT	TCTTTTCTAC AGAAAAGATG		*	•
3401	ACGTTAAGGG TGCAATTCCC	ATTTTGGTCA TAAAACCAGT	•	· ·	
3451	TCCTTTTAAA	TTAAAAATGA AATTTTTACT	• *		
	TAAACTTGGT ATTTGAACCA	-			
3551	AGCGATCTGT TCGCTAGACA	CTATTTCGTT GATAAAGCAA			
3601	AGATAACTAC TCTATTGATG	GATACGGGAG CTATGCCCTC			
3651		ACCCACGCTC TGGGTGCGAG			
3701	. =	AJGGCCGAGC TCCCGGCTCG	_		TTATCCGCCT AATAGGCGGA

36/56 F/G. 19. (CONTINUED)

3751		TATTAATTGT ATAATTAACA	· -		
3801		TGCGCAACGT ACGCGTTGCA			
3851		TTTGGTATGG AAACCATACC			
3901	GGCGAGTTAC CCGCTCAATG	ATGATCCCCC TACTAGGGGG			
3951	GGTCCTCCGA CCAGGAGGCT	TCGTTGTCAG AGCAACAGTC			
4001		GCACTGCATA CGTGACGTAT			•
4051		GACTGGTGAG CTGACCACTC			
4101		CGAGTTGCTC GCTCAACGAG			
4151	••••	AGAACTTTAA TCTTGAAATT	•		·
4201	·	CTCAAGGATC GAGTTCCTAG	•		-
4251		CACCCAACTG GTGGGTTGAC			·
4301		GCAAAAACAG CGTTTTTGTC			AAGGGAATAA TTCCCTTATT
4351		GAAATGTTGA CTTTACAACT			
4401	TGAAGCATTT ACTTCGTAAA	• :	TTGTCTCATG AACAGAGTAC	•	
4451	• • • • •	AATAAACAAA TTATTTGTTT		•	
4501	<u>.</u>	CGCGCCCTGT GCGCGGGACA			
4551		GCGTGACCGC CGCACTGGCG			
4601	• • • • • • • •	TTCCCTTCCT AAGGGAAGGA			
4651		TCGGGGGCTC AGCCCCCGAG			

FIG. 19. (CONTINUED)

4701	CACCTCGACC	CCAAAAAACT	TGATTAGGGT	GATGGTTCAC	GTAGTGGGCC
	GTGGAGCTGG	GGTTTTTTGA	ACTAATCCCA	CTACCAAGTG	CATCACCCGG
4751	ATCGCCCTGA	TAGACGGTTT	ттссссттт	GACGTTGGAG	TCCACGTTCT
			AAGCGGGAAA	•	
•		•			
4801	TTAATAGTGG	ACTCTTGTTC	CAAACTGGAA	CAACACTCAA	CCCTATCTCG
	AATTATCACC	TGAGAACAAG	GTTTGACCTT	GTTGTGAGTT	GGGATAGAGC
4851	GTCTATTCTT	ምም ርል ጥጥልጥል	ΔGGGΔTTTTG	СССАТТТССС	$CCT\Delta TTCCTT$
1001			TCCCTAAAAC		
					·
4901	AAAAAATGAG	CTGATTTAAC	AAAAATTTAA	CGCGAATTTT	AACAAAATAT
	TTTTTTACTC	GACTAAATTG	TTTTTAAATT	GCGCTTAAAA	TTGTTTTATA
• • •		•			
4951	TAACGTTTAC				
•	ATTGCAAATG	TTAAAGGGTA	AGCGGTAAGT	CCGACGCGTT	GACAACCCTT
5001	GGGCGATCGG	TOCOCOCOTO	ጥጥ /////	CCCCACCCCA	ስርር ጥ ስርርስጥር
2001	2000 19 15 15 15 15 15 15 15 15 15 15 15 15 15	•	AAGCGATAAT		
. · .	COCGCIAGCO	ACGCCCGAG	ANGCGAIAAI	3003103331	ICGAIGGIAC
5051	ATAAGTAAGT	AATATTAAGG	TACGGGAGGT	ACTTGGAGCG	GCCGCAATAA
	TATTCATTCA	TTATAATTCC	ATGCCCTCCA	TGAACCTCGC	CGGCGTTATT
				-	
5101	AATATCTTTA				
••	TTATAGAAAT	AAAAGTAATG	TAGACACACA	ACCAAAAAAC	ACACTTAGCT
5151	TAGTACTAAC	אימרכרייריי	CATCAAAACA	DADCCDADCD	מממממממ
ŢŢŢ	a 🌺 😘 a rate of a figure of the contract of		GTAGTTTTGT		
5201	GCAAAATAGG	CTGTCCCCAG	TGCAAGTGCA	GGTGCCAGAA	CATTTCTCTA
	CGTTTTATCC	GACAGGGGTC	ACGTTCACGT	CCACGGTCTT	GTAAAGAGAT
5251	TCGATA	-	•		
	0 (' (' III				

FIG. 20.

38/56

Blot 4

Blot 3

Blot 2

Blot 1

1 2 3

CED-6

FIG. 21.

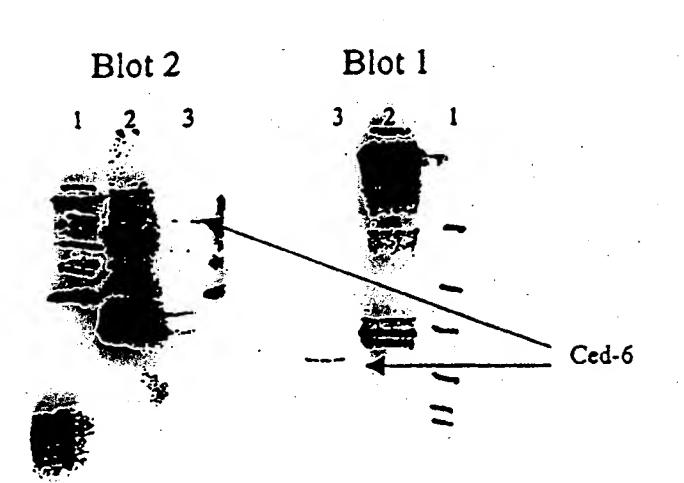


FIG. 22.

Blot 8

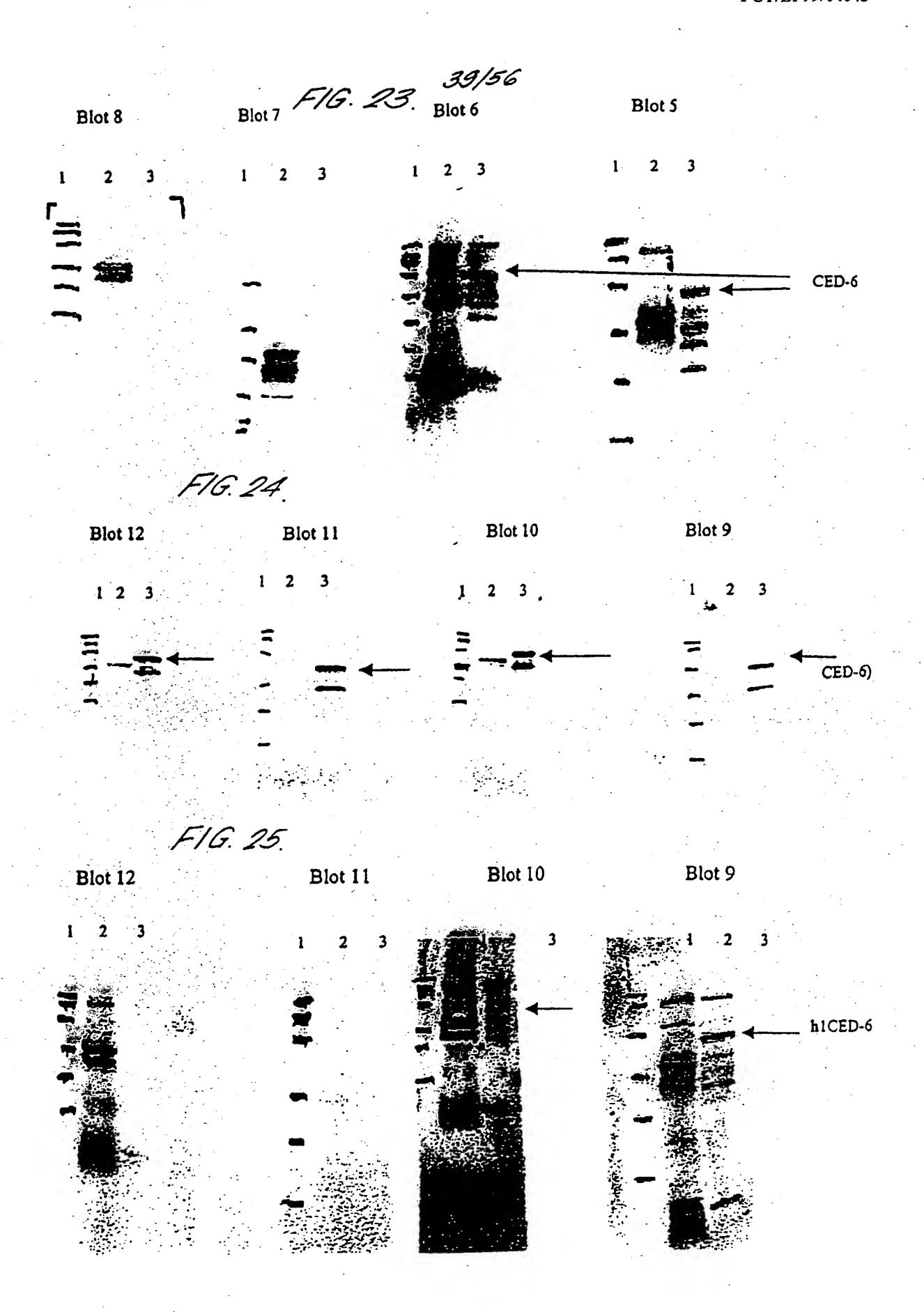
Blot 7

Blot 6

Blot 5

1 2 3 3

h1CED-6



WO 99/64586 PCT/EP99/04043

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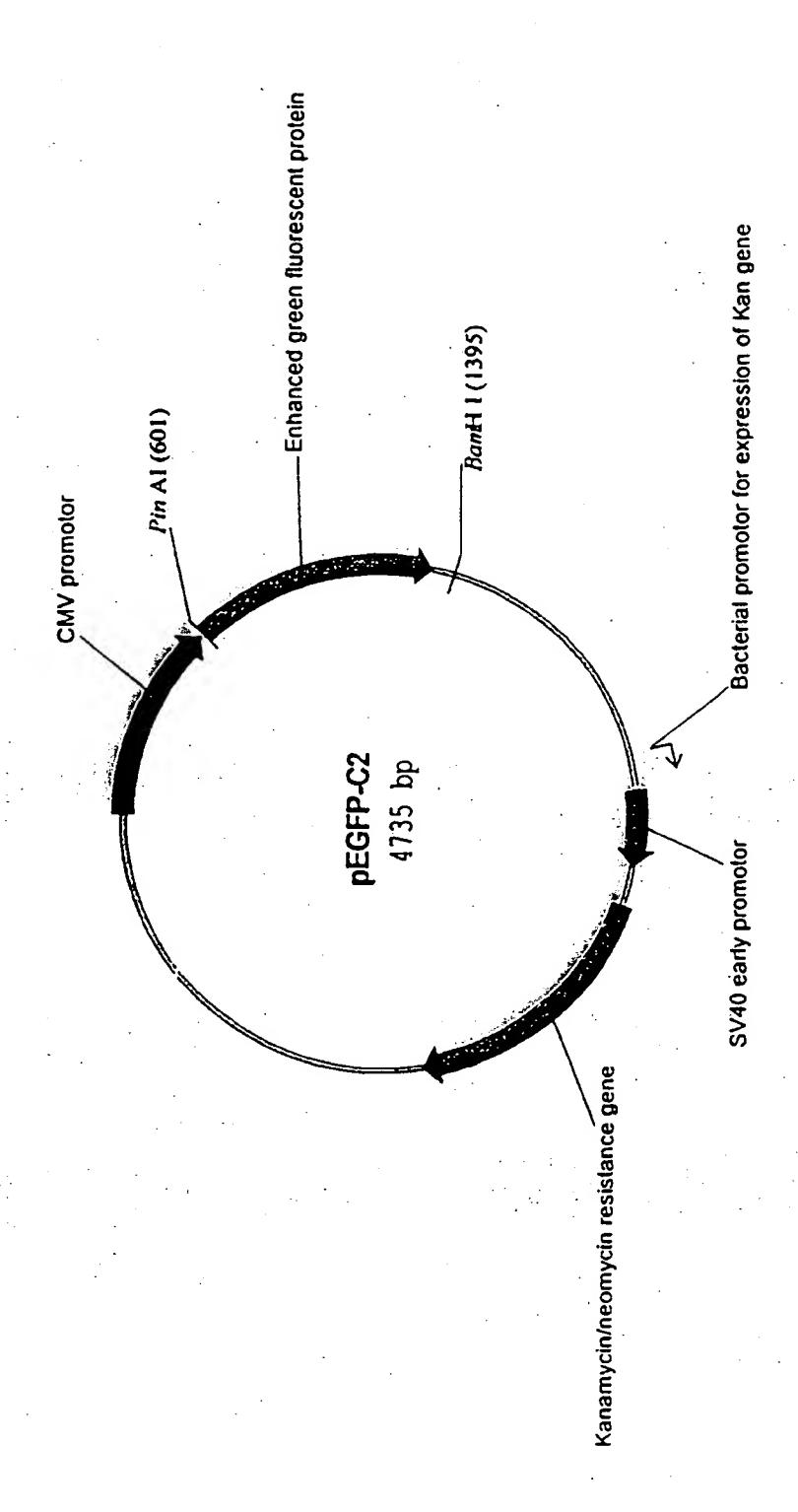
SQ	SEQUENCE	4735 BP				
60	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC	ATTAGTTCAT	AGCCCATATA	TGGAGTTCCG
120	CGTTACATAA	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG	CCCAACGACC	CCCGCCCATT
180	GACGTCAATA	ATGACGTATG	TTCCCATAGT	AACGCCAATA	GGGACTTTCC	ATTGACGTCA
240	ATGGGTGGAG	TATTTACGGT	AAACTGCCCA	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC
	AAGTACGCCC	CCTATTGACG	TCAATGACGG	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA
300	CATGACCTTA	TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA	TCGCTATTAC
36 0	CATGGTGATG	CGGTTTTGGC	AGTACATCAA	TGGGCGTGGA	TAGCGGTTTG	ACTCACGGGG.
420						•
480	ATTTCCAAGT	CTCCACCCCA	TTGACGTCAA	TGGGAGTTTG	TTTTGGCACC	AAAATCAACG
540	GGACTTTCCA	AAATGTCGTA	ACAACTCCGC	CCCATTGACG	CAAATGGGCG	GTAGGCGTGT
600	ACGGTGGGAG	GTCTATATAA	GCAGAGCTGG	TTTAGTGAAC	CGTCAGATCC	GCTAGCGCTA
6 60	CCGGTCGCCA	CCATGGTGAG	CAAGGGCGAG	GAGCTGTTCA	CCGGGGTGGŤ	GCCCATCCTG
	GTCGAGCTGG	ACGGCGACGT	AAACGGCCAC	AAGTTCAGCG	TGTCCGGCGA	GGGCGAGGGC
720 780	GATGCCACCT	ACGGCAAGCT	GACCCTGAAG	TTCATCTGCA	CCACCGGCAA	GCTGCCCGTG
840	CCCTGGCCCA	CCCTCGTGAC	CACCCTGACC	TACGGCGTGC	AGTGCTTCAG	CCGCTACCCC
900	GACCACATGA	AGCAGCACGA	CTTCTTCAAG	TCCGCCATGC	CCGAAGGCTA	CGTCCAGGAG
960	CGCACCATCT	TCTTCAAGGA	CGACGGCAAC	TACAAGACCC	GCGCCGAGGT	GAAGTTCGAG
1020	GGCGACACCC	TGGTGAACCG	CATCGAGCTG	AAGGGCATCG	ACTTCAAGGA	GGACGGCAAC
	ATCCTGGGGC	ACAAGCTGGA	GTACAACTAC	AACAGCCACA	ACGTCTATAT	CATGGCCGAC
1080	AAGCAGAAGA	ACGCCATCAA	GGTGAACTTC	AAGATCCGCC	ACAACATCGA	GGACGGCAGC
1140	GTGCAGCTCG	CCGACCACTA	CCAGCAGAAC	ACCCCCATCG	GCGACGGCCC	CGTGCTGCTG
1200	CCCGACAACC	ACTACCTGAG	CACCCAGTCC	GCCCTGAGCA	AAGACCCCAA	CGAGAAGCGC
1260	GATCACATGG	тестестева	GTTCGTGACC	GCCGCCGGGA	тсастстска	САТССАССАС
1320						
1380	CTGTACAAGT	CCGGCCGGAC	TCAGATCTCG	AGCTCAAGCT	TCGAATTCTG	CAGTCGACGG
1440	TACCGCGGGC	CCGGGATCCA	CCGGATCTAG	ATAACTGATC	ATAATCAGCC	ATACCACATT
1500	TGTAGAGGTT	TTACTTGCTT	TAAAAAACCT	CCCACACCTC	CCCCTGAACC	TGAAACATAA
	AATGAATGCA	ATTGTTGTTG	TTAACTTGTT	TATTGCAGCT	TATAATGGTT	ACAAATAAAG
1560						

41/56 F/G. 26. (CONTINUED)

1620	•	ACAAATTTCA	CAAATAAAGC	ATTTTTTCA	CTGCATTCTA	GTTGTGGTTT
(·)	·	ATCAATGTAT	CTTAACGCGT	AAATTGTAAG	CGTTAATATT	TTGTTAAAAT
1680	TCGCGTTAAA	TTTTTGTTAA	ATCAGCTCAT	TTTTTAACCA	ATAGGCCGAA	ATCGGCAAAA
1740	TCCCTTATAA	ATCAAAAGAA	TAGACCGAGA	TAGGGTTGAG	TGTTGTTCCA	GTTTGGAACA
1800	AGAGTCCACT	ATTAAAGAAC	GTGGACTCCA	ACGTCAAAGG	GCGAAAAACC	GTCTATCAGG
1860	GCGATGGCCC	ACTACGTGAA	CCATCACCCT	AATCAAGTTT	TTTGGGGTCG	AGGTGCCGTA
1920	AAGCACTAAA	тсссаассст	AAAGGGAGCC	CCCGATTTAG	AGCTTGACGG	GGAAAGCCGG
1980						
2040			GGGAAGAAAG			
2100	GTGTAGCGGT	CACGCTGCGC	GTAACCACCA	CACCCGCCGC	GCTTAATGCG	CCGCTACAGG
2160	GCGCGTCAGG	TGGCACTTTT	CGGGGAAATG	TGCGCGGAAC	CCCTATTTGT	TTATTTTTCT
2220	AAATACATTC	AAATATGTAT	CCGCTCATGA	GACAATAACC	CTGATAAATG	CTTCAATAAT
2280	ATTGAAAAAG	GAAGAGTCCT	GAGGCGGAAA	GAACCAGCTG	TGGAATGTGT	GTCAGTTAGG
	GTGTGGAAAG	TCCCCAGGCT	CCCCAGCAGG	CAGAAGTATG	CAAAGCATGC	ATCTCAATTA
2340	GTCAGCAACC	AGGTGTGGAA	AGTCCCCAGG	CTCCCCAGCA	GGCAGAAGTA	TGCAAAGCAT
2400	GCATCTCAAT	TAGTCAGCAA	CCATAGTCCC	GCCCCTAACT	CCGCCCATCC	CGCCCTAAC
2460	TCCGCCCAGT	TCCGCCCATT	CTCCGCCCCA	TGGCTGACTA	ATTTTTTTA	TTTATGCAGA
2520	GGCCGAGGCC	GCCTCGGCCT	CTGAGCTATT	CCAGAAGTAG	TGAGGAGGCT	TTTTTGGAGG
2580			GATCAAGAGA			• •
2640			·			
2700			TCTCCGGCCG			
2760	GGGCACAACA	GACAATCGGC	TGCTCTGATG	CCGCCGTGTT	CCGGCTGTCA	GCGCAGGGC
2820	GCCCGGTTCT	TTTTGTCAAG	ACCGACCTGT	CCGGTGCCCT	GAATGAACTG	CAAGACGAGG
2880	CAGCGCGGCT	ATCGTGGCTG	GCCACGACGG	GCGTTCCTTG	CGCAGCTGTG	CTCGACGTTG
2940	TCACTGAAGC	GGGAAGGGAC	TGGCTGCTAT	TGGGCGAAGT	GCCGGGGCAG	GATCTCCTGT
	CATCTCACCT	TGCTCCTGCC	GAGAAAGTAT	CCATCATGGC	TGATGCAATG	CGGCGGCTGC
3000	ATACGCTTGA	TCCGGCTACC	TGCCCATTCG	ACCACCAAGC	GAAACATCGC	ATCGAGCGAG
30,60	CACGTACTCG	GATGGAAGCC	GGTCTTGTCG	ATCAGGATGA	TCTGGACGAA	GAGCATCAGG
3120	GGCTCGCGCC	AGCCGAACTG	TTCGCCAGGC	TCAAGGCGAG	CATGCCCGAC	GGCGAGGATC
3180			GCCTGCTTGC			
3240	TOGICGIGAC	COR. GOCGRI	GCC1GC11GC	COMMINICAL	JULIOGRAMI	GGCCGCTTT

42/56 F/G. 26. (CONTINUED)

3300		CGACTGTGGC	CGGCTGGGTG	TGGCGGACCG	CTATCAGGAC	ATAGCGTTGG
	CTACCCGTGA	TATTGCTGAA	GAGCTTGGCG	GCGAATGGGC	TGACCGCTTC	CTCGTGCTTT
3360		CGCTCCCGAT	TCGCAGCGCA	TCGCCTTCTA	TCGCCTTCTT	GACGAGTTCT
3420	TCTGAGCGGG	ACTCTGGGGT	TCGAAATGAC	CGACCAAGCG	ACGCCCAACC	TGCCATCACG
3480	AGATTTCGAT	TCCACCGCCG	CCTTCTATGA	AAGGTTGGGC	TTCGGAATCG	TTTTCCGGGA
3540			AGCGCGGGGA			
3600						
3660			GGAAGGAGAC			
3720	AATAAAAAGA	CAGAATAAAA	CGCACGGTGT	TGGGTCGTTT	GTTCATAAAC	GCGGGGTTCG
3780	GTCCCAGGGC	TGGCACTCTG	TCGATACCCC	ACCGAGACCC	CATTGGGGCC	AATACGCCCG
3840	CGTTTCTTCC	TTTTCCCCAC	CCCACCCCC	AAGTTCGGGT	GAAGGCCCAG	GGCTCGCAGC
3900	CAACGTCGGG	GCGGCAGGCC	CTGCCATAGC	CTCAGGTTAC	TCATATATAC	TTTAGATTGA
	TTTAAAACTT	CATTTTTAAT	TTAAAAGGAT	CTAGGTGAAG	ATCCTTTTTG	ATAATCTCAT
3960	GACCAAAATC	CCTTAACGTG	AGTTTTCGTT	CCACTGAGCG	TCAGACCCCG	TAGAAAAGAT
4020	CAAAGGATCT	TCTTGAGATC	CTTTTTTTCT	GCGCGTAATC	TGCTGCTTGC	AAACAAAAA
4080	ACCACCGCTA	CCAGCGGTGG	TTTGTTTGCC	GGATCAAGAG	CTACCAACTC	TTTTTCCGAA
4140			CGCAGATACC	·		<i>i</i> .
4200						
4260			CTGTAGCACC	•		
4320	ACCAGTGGCT	GCTGCCAGTG	GCGATAAGTC	GTGTCTTACC	GGGTTGGACT	CAAGACGATA
4380	GTTACCGGAT	AAGGCGCAGC	GGTCGGGCTG	AACGGGGGGT	TCGTGCACAC	AGCCCAGCTT
4440	GGAGCGAACG	ACCTACACCG	AACTGAGATA	CCTACAGCGT	GAGCTATGAG	AAAGCGCCAC
	GCTTCCCGAA	GGGAGAAAGG	CGGACAGGTA	TCCGGTAAGC	GGCAGGGTCG	GAACAGGAGA
4500	GCGCACGAGG	GAGCTTCCAG	GGGGAAACGC	CTGGTATCTT	TATAGTCCTG	TCGGGTTTCG
4560	CCACCTCTGA	CTTGAGCGTC	GATTTTTGTG	ATGCTCGTCA	GGGGGGCGGA	GCCTATGGAA
4620	AAACGCCAGC	AACGCGGCCT	TTTTACGGTT	CCTGGCCTTT	TGCTGGCCTT	TTGCTCACAT
4680			CTGATTCTGT			
4735 //			CIGNITOIGI	GONIANCOL	ATTACCGCCA	IGCMI



F16.27

44/56 F/G. 28.

SQ	SEQUENCE TCGACGGTAC	5628 BP CGCGGGCCCG	GGATCCACCG	GATCTAGATA	ACTGATCATA	ATCAGCCATA
60					ACACCTCCCC	
120						
180					TGCAGCTTAT	
240		·			TTTTTCACTG	
300	GTGGTTTGTC	CAAACTCATC	AATGTATCTT	AACGCGTAAA	TTGTAAGCGT	TAATATTTTG
360	TTAAAATTCG	CGTTAAATTT	TTGTTAAATC	AGCTCATTTT	TTAACCAATA	GGCCGAAATC
420	GGCAAAATCC	CTTAȚAAATC	AAAAGAATAG	ACCGAGATAG	GGTTGAGTGT	TGTTCCAGTT
480	TGGAACAAGA	GTCCACTATT	AAAGAACGTG	GACTCCAACG	TCAAAGGGCG	AAAAACCGTC
	TATCAGGGCG	ATGGCCCACT	ACGTGAACCA	TCACCCTAAT	CAAGTTTTTT	GGGGTCGAGG
540	TGCCGTAAAG	CACTAAATCG	GAACCCTAAA	GGGAGCCCCC	GATTTAGAGC	TTGACGGGGA
600	AAGCCGGCGA	ACGTGGCGAG	AAAGGAAGGG	AAGAAAGCGA	AAGGAGCGGG	CGCTAGGGCG
660	CTGGCAAGTG	TAGCGGTCAC	GCTGCGCGTA	ACCACCACAC	CCGCCGCGCT	TAATGCGCCG
720		•		·	GCGGAACCCC	
780	. •				AATAACCCTG	
340						
900					CCAGCTGTGG	·
960	AGTTAGGGTG	TGGAAAGTCC	CCAGGCTCCC	CAGCAGGCAG	AAGTATGCAA	AGCATGCATC
1020	TCAATTAGTC	AGCAACCAGG	TGTGGAAAGT	CCCCAGGCTC	CCCAGCAGGC	AGAAGTATGC
080	AAAGCATGCA	TCTCAATTAG	TCAGCAACCA	TAGTCCCGCC	CCTAACTCCG	CCCATCCCGC
140	CCCTAACTCC	GCCCAGTTCC	GCCCATTCTC	CGCCCCATGG	CTGACTAATT	TTTTTTTTTT
	ATGCAGAGGC	CGAGGCCGCC	TCGGCCTCTG	AGCTATTCCA	GAAGTAGTGA	GGAGGCTTTT
.200	TTGGAGGCCT	AGGCTTTTGC	AAAGATCGAT	CAAGAGACAG	GATGAGGATC	GTTTCGCATG
.260	ATTGAACAAG		•		•	÷ .
.320	TATGACTGGG		•			
380						
440	CAGGGGCGCC					. –
500	GACGAGGCAG	CGCGGCTATC	GTGGCTGGCC	ACGACGGGCG	TTCCTTGCGC	AGCTGTGCTC

45/56 FIG. 28. (CONTINUED)

1560		CTGAAGCGGG	AAGGGACTGG	CTGCTATTGG	GCGAAGTGCC	GGGGCAGGAT
1620		CTCACCTTGC	TCCTGCCGAG	AAAGTATCCA	TCATGGCTGA	TGCAATGCGG
1680	CGGCTGCATA	CGCTTGATCC	GGCTACCTGC	CCATTCGACC	ACCAAGCGAA	ACATCGCATC
1740	GAGCGAGCAC	GTACTCGGAT	GGAAGCCGGT	CTTGTCGATC	AGGATGATCT	GGACGAAGAG
•	CATCAGGGGC	TCGCGCCAGC	CGAACTGTTC	GCCAGGCTCA	AGGCGAGCAT	GCCCGACGGC
1800	GAGGATCTCG	TCGTGACCCA	TGGCGATGCC	TGCTTGCCGA	ATATCATGGT	GGAAAATGGC
1860	CGCTTTTCTG	GATTCATCGA	CTGTGGCCGG	CTGGGTGTGG	CGGACCGCTA	TCAGGACATA
1920	GCGTTGGCTA	CCCGTGATAT	TGCTGAAGAG	CTTGGCGGCG	AATGGGCTGA	CCGCTTCCTC
1980		GTATCGCCGC	TCCCGATTCG	CAGCGCATCG	CCTTCTATCĠ	CCTTCTTGAC
2040	GAGTTCTTCT	GAGCGGGACT	CTGGGGTTCG	AAATGACCGA	CCAAGCGACG	CCCAACCTGC
2100			ACCGCCGCCT			
2160			ATCCTCCAGC			:
2220			GAAACACGGA	·	,	
2280						
2340			AATAAAACGC			
2400			CACTCTGTCG			
2460	ACGCCCGCGT	TTCTTCCTTT	TCCCCACCCC	ACCCCCAAG	TTCGGGTGAA	GGCCCAGGGC
2520	TCGCAGCCAA	CGTCGGGGCG	GCAGGCCCTG	CCATAGCCTC	AGGTTACTCA	TATATACTTT
2580	AGATTGATTT	AAAACTTCAT	TTTTAATTTA	AAAGGATCTA	GGTGAAGATC	CTTTTTGATA
2640	ATCTCATGAC	CAAAATCCCT	TAACGTGAGT	TTTCGTTCCA	CTGAGCGTCA	GACCCCGTAG
2700	AAAAGATCAA	AGGATCTTCT	TGAGATCCTT	TTTTTCTGCG	CGTAATCTGC	TGCTTGCAAA
	· 人名英格兰	ACCGCTACCA	GCGGTGGTTT	GTTTGCCGGA	TCAAGAGCTA	CCAACTCTTT
2760		AACTGGCTTC	AGCAGAGCGC	AGATACCAAA	TACTGTCCTT	CTAGTGTAGC
2820	CGTAGTTAGG	CCACCACTTC	AAGAACTCTG	TAGCACCGCC	TACATACCTC	GCTCTGCTAA
2880	TCCTGTTACC	AGTGGCTGCT	GCCAGTGGCG	ATAAGTCGTG	TCTTACCGGG	TTGGACTCAA
2940	GACGATAGTT	ACCGGATAAG	GCGCAGCGGT	CGGGCTGAAC	GGGGGTTCG	TGCACACAGC
3000	CCAGCTTGGA	GCGAACGACC-	TACACCGAAC	TGAGATACCT	ACAGCGTGAG	CTATGAGAAA
3060			AGAAAGGCGG			
3120			CTTCCAGGGG			
3180	UJUNUNDDO	ORUGANA	CIICCAGGGG	unnacuccity (GIAICIIIAI .	UG 1 C C 1 G 1 C G

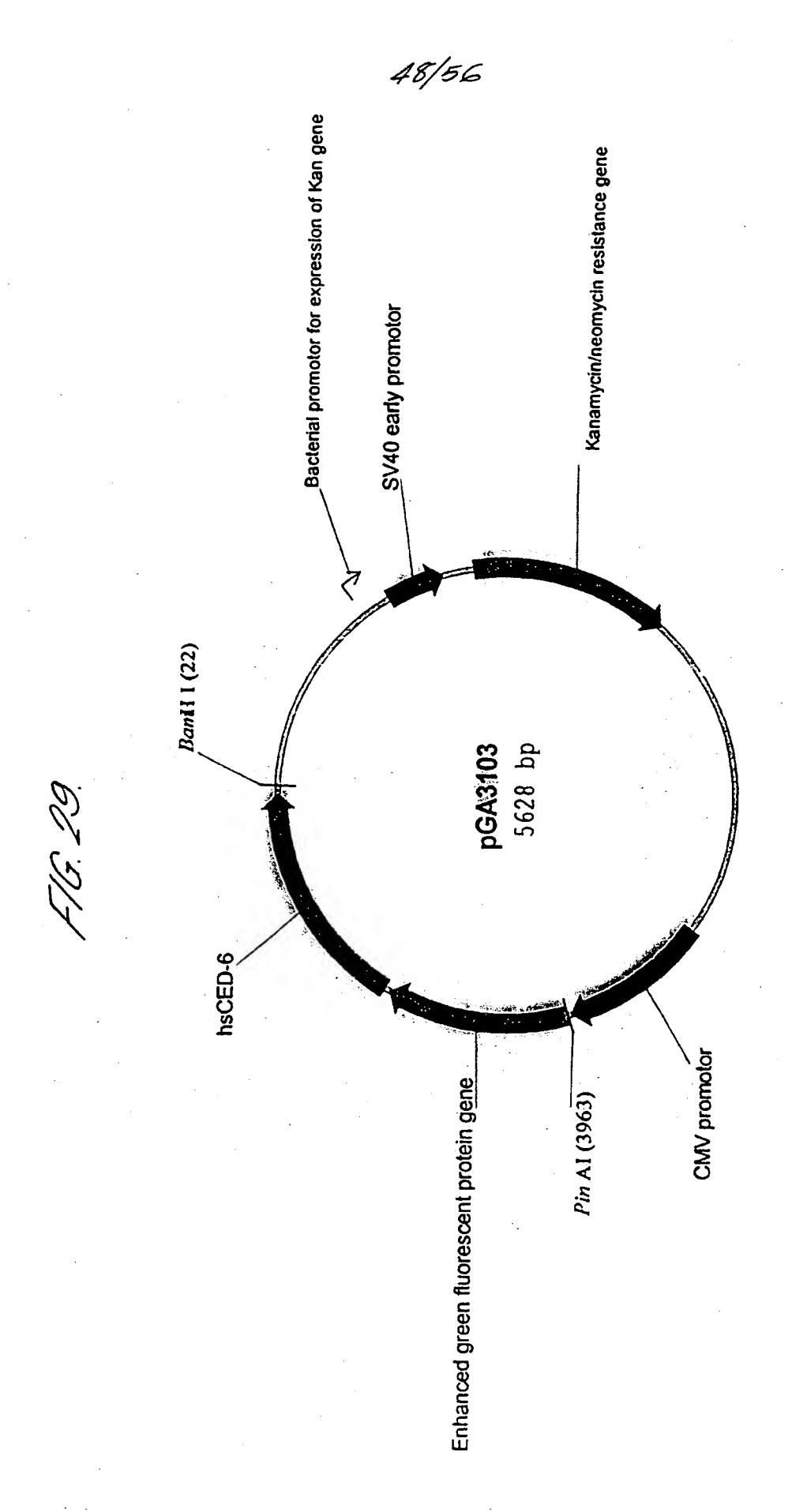
46/56 FIG. 28. (CONTINUED) -

		A CCTCTGACTI	GAGCGTCGAT	TTTTGTGAT	G CTCGTCAGGG	GGGCGGAGCC
3240	-	CGCCAGCAA	C GCGGCCTTTI	TACGGTTCCT	GGCCTTTTGC	TGGCCTTTTG
3300		CTTTCCTGC	TTATCCCCTG	ATTCTGTGGA	TAACCGTATT	' ACCGCCATGC
3360)				ATAGCCCATA	
3420)	•			CGCCCAACGA	
3480)					•
3540				•	TAGGGACTTT	
3600					TACATCAAGT	
3660		CCCCTATTGA	CGTCAATGAC	GGTAAATGGC	CCGCCTGGCA	TTATGCCCAG
3720		TATGGGACTT	TCCTACTTGG	CAGTACATCT	ACGTATTAGŤ	CATCGCTATT
3780		TGCGGTTTTG	GCAGTACATC	AATGGGCGTG	GATAGCGGTT	TGACTCACGG
3840	GGATTTCCAA	GTCTCCACCC	CATTGACGTC	AATGGGAGTT	TGTTTTGGCA	CCAAAATCAA
		CAAAATGTCG	TAACAACTCC	GCCCCATTGA	CGCAAATGGG	CGGTAGGCGT
3900	GTACGGTGGG	AGGTCTATAT	AAGCAGAGCT	GGTTTAGTGA	ACCGTCAGAT	CCGCTAGCGC
3960	TACCGGTCGC	CACCATGGTG	AGCAAGGGCG	AGGAGCTGTT	CACCGGGGTG	GTGCCCATCC
4020	,	•			CGTGTCCGGC	
4080					CACCACCGGC	•
4140	•	•	•			
4200					GCAGTGCTTC	
4260					GCCCGAAGGC	
4320	AGCGCACCAT	CTTCTTCAAG	GACGACGGCA	ACTACAAGAC	CCGCGCCGAG	GTGAAGTTCG
4380	AGGGCGACAC	CCTGGTGAAC	CGCATCGAGC	TGAAGGCAT	CGACTTCAAG	GAGGACGGCA
4440	ACATCCTGGG	GCACAAGCTG	GAGTACAACT	ACAACAGCCA	CAACGTCTAT	ATCATGGCCG
4500	ACAAGCAGAA	GAACGGCATC	AAGGTGAACT	TCAAGATCCG	CCACAACATC	GAGGACGGCA
	GCGTGCAGCT	CGCCGACCAC	TACCAGCAGA	ACACCCCCAT	CGGCGACGGC	CCCGTGCTGC
4560	TGCCCGACAA	CCACTACCTG	AGCACCCAGT	CCGCCCTGAG	CAAAGACCCC	AACGAGAAGC
4620	GCGATCACAT	GGTCCTGCTG	GAGTTCGTGA	CCGCCGCCGG	GATCACTCTC	GGCATGGACG
4680		·			TGCTTTTAGC	
4740			,		TTTCATTCCC	
4800						
4860	NOTE I CITUS	CAGIACAGAA	G I GGAACAGC	CAAAAGGAAC	AGAAGTTGTG	AGAGATGCTG

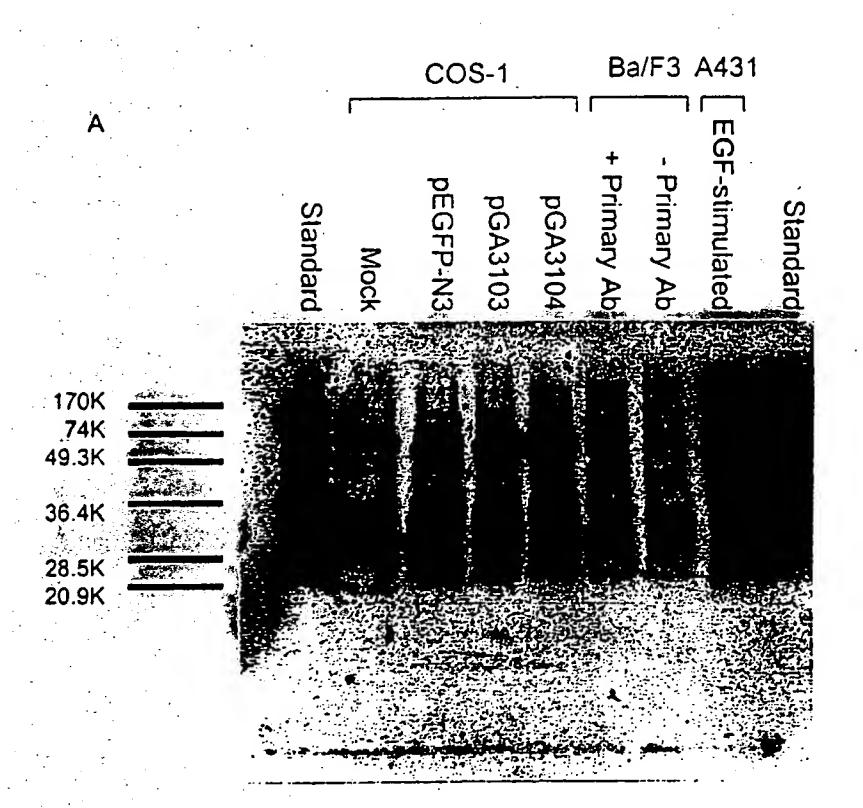
FIG. 28. (CONTINUED)

TAAGGAAACT AAAGTTTGCA AGACATATCA AGAAATCTGA AGGCCAGAAA ATTCCTAAAG

4920 TGGAGTTGCA AATATCAATT TATGGAGTAA AAATTCTAGA ACCCAAAACA AAGGAAGTTC 4980 AACACAATTG CCAGCTTCAT AGAATATCTT TTTGTGCAGA TGATAAAACT GACAAGAGGA 5040 TATTCACTTT CATATGCAAA GATTCTGAGT CAAATAAACA TTTGTGCTAT GTATTTGACA 5100 GCGAAAAGTG TGCTGAAGAG ATCACTTTAA CAATTGGCCA AGCATTTGAC CTGGCATACA 5160 CGAAATTTCT AGAATCAGGA GGAAAAGATG TTGAAACAAG AAAACAGATC GCAGGGTTAC 5220 AAAAAÄGAAT CCAAGACTTA GAAACAGAAA ATATGGAACT TAAAAATAAA GTACAAGATT TGGAAAACCA ACTGAGAATA ACTCAAGTAT CAGCACCTCC AGCAGGCAGT ATGACACCTA 5340 5400 CGATGCCTAC TCGCAATGGC ACACAGCCAC CTCCAGTACC TAGTAGATCT ACTGAGATTA 5460 AACGGGACCT GTTTGGAGCA GAACCTTTTG ACCCATTTAA CTGTGGAGCA GCAGATTTCC 5520 CTCCAGATAT TCAATCAAAA TTAGATGAGA TGCAGGAGGG GTTCAAAATG GGACTAACTC 5580 TTGAAGGCAC AGTATTTTGT CTCGACCCGT TAGACAGTAG GTGCTGAG 5628



F1G. 30.



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FIG. 30. (CONTINUED)

			CO	S-1		Ba	3/F3	A431	
B	Standard	Mock	pEGFP-N3	pGA3103	pGA3104	+ Primary Ab	- Primary Ab	_EGF-stimulated	Standard
170K 74K 49.3K	,			ة نس	=	The state of the s			
36.4K	TO		•						
28.5K 20.9K	و ها فصيحين ي								

FIG. 30. (CONTINUED)

28.5K

20.9K

		CO	S-1	Ba/F3	A431	
C	Standard	~ pEGFP-N3 Mock	pGA3104 pGA3103	- Primary Ab + Primary Ab	EGF-stimulated	Standard
170K	· ·					-
49.3K	_					
36.4K	1-110					

51/56 F/G. 31.

SQ SEQUENCE 6121 BP GATCTATGGG CTGTGACCGG AACTGTGGGC TCATCGCTGG GGCTGTCATT GGTGCTGTCC 60 TGGCTGTGTT TGGAGGTATT CTAATGCCAG TTGGAGACCT GCTTATCCAG AAGACAATTA 120 AAAAGCAAGT TGTCCTCGAA GAAGGTACAA TTGCTTTTAA AAATTGGGTT AAAACAGGCA 180 CAGAAGTTTA CAGACAGTTT TGGATCTTTG ATGTGCAAAA TCCACAGGAA GTGATGATGA 240 ACAGCAGCAA CATTCAAGTT AAGCAAAGAG GTCCTTATAC GTACAGAGTT CGTTTTCTAG 300 CCAAGGAAAA TGTAACCCAG GACGCTGAGG ACAACACAGT CTCTTTCCTG CAGCCCAATG 360 GTGCCATCTT CGAACCTTCA CTATCAGTTG GAACAGAGGC TGACAACTTC ACAGTTCTCA 420 ATCTGGCTGT GGCAGCTGCA TCCCATATCT ATCAAAATCA ATTTGTTCAA ATGATCCTCA 480 ATTCACTTAT TAACAAGTCA AAATCTTCTA TGTTCCAAGT CAGAACTTTG AGAGAACTGT 540 TATGGGGCTA TAGGGATCCA TTTTTGAGTT TGGTTCCGTA CCCTGTTACT ACTACAGTTG 600 GTCTGTTTTA TCCTTACAAC AATACTGCAG ATGGAGTTTA TAAAGTTTTC AATGGAAAAG 660 ATAACATAAG TAAAGTTGCC ATAATCGACA CATATAAAGG TAAAAGGAAT CTGTCCTATT 720... GGGAAAGTCA CTGCGACATG ATTAATGGTA CAGATGCAGC CTCATTTCCA CCTTTTGTTG 780 AGAAAAGCCA GGTATTGCAG TTCTTTTCTT CTGATATTTG CAGGTCAATC TATGCTGTAT 840 TTGAATCCGA CGTTAATCTG AAAGGAATCC CTGTGTATAG ATTCGTTCTT CCATCCAAGG 900 CCTTTGCCTC TCCAGTTGAA AACCCAGACA ACTATTGTTT CTGCACAGAA AAAATTATCT 960 CAAAAATTG TACATCATAT GGTGTGCTAG ACATCAGCAA ATGCAAAGAA GGGAGACCTG 1020 TGTACATTTC ACTTCCTCAT TTTCTGTATG CAAGTCCTGA TGTTTCAGAA CCTATTGATG 1080 GATTAAACCC AAATGAAGAA GAACATAGGA CATACTTGGA TATTCAACCT ATAACTGGAT 1140 TCACTTTACA ATTTGCAAAA CGGCTGCAGG TCAACCTATT GGTCAAGCCA TCAGAAAAA 1200 TTCAAGTATT AAAGAATCTG AAGAGGAACT ATATTGTGCC TATTCTTTGG CTTAATGAGA 1260 CTGGGACCAT TGGTGATGAG AAGGCAAACA TGTTCAGAAG TCAAGTAACT GGAAAAATAA 1320 ACCTCCTTGG CCTGATAGAA ATGATCTTAC TCAGTGTTGG TGTGGTGATG TTTGTTGCTT 1380 TTATGATTTC ATATTGTGCA TGCAGATCGA AAACAATAAA AGTCGACGGT ACCGCGGGCC 1440 CGGGATCCAT CGCCACCATG GTGAGCAAGG GCGAGGAGCT GTTCACCGGG GTGGTGCCCA 1500

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1560	TCCTGGTCGA	GCTGGACGGC	GACGTAAACG	GCCACAAGTT	CAGCGTGTCC	GGCGAGGGCG
	AGGGCGATGC	CACCTACGGC	AAGCTGACCC	TGAAGTTCAT	CTGCACCACC	GGCAAGCTGC
1620	CCGTGCCCTG	GCCCACCCTC	GTGACCACCC	TGACCTACGG	CGTGCAGTGC	TTCAGCCGCT
1680	ACCCCGACCA	CATGAAGCAG	CACGACTTCT	TCAAGTCCGC	CATGCCCGAA	GGCTACGTCC
1740	AGGAGCGCAC	CATCTTCTTC	AAGGACGACG	GCAACTACAA	GACCCGCGCC	GAGGTGAAGT
1800	TCGAGGGCGA	CACCCTGGTG	AACCGCATCG	AGCTGAAGGG	CATCGACTTC	AAGGAGGACG
1860	GCAACATCCT	GGGGCACAAG	CTGGAGTACA	ACTACAACAG	CCACAACGTC	TATATCATGG
1920	CCGACAAGCA	GAAGAACGGC	ATCAAGGTGA	ACTTCAAGAT	CCGCCACAAC	ATCGAGGACG
1980	GCAGCGTGCA	GCTCGCCGAC	CACTACCAGC	AGAACACCCC	CATCGGCGAC	GGCCCCGTGC
2040	TGCTGCCCGA	CAACCACTAC	CTGAGCACCC	AGTCCGCCCT	GAGCAAAGAC	CCCAACGAGA
2100	AGCGCGATCA	CATGGTCCTG	CTGGAGTTCG	TGACCGCCGC	CGGGATCACT	CTCGGCATGG
2160	ACGAGCTGTA	CAAGTAAAGC	GGCCGCGACT	CTAGATCATA	ATCAGCCATA	CCACATTTGT
2220	AGAGGTTTTA	CTTGCTTTAA	AAAACCTCCC	ACACCTCCCC	CTGAACCTGA	AACATAAAAT
2280	GAATGCAATT	GTTGTTGTTA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA	AATAAAGCAA
2340			ATAAAGCATT		CATTCTAGTT	GTGGTTTGTC
2400			AAGGCGTAAA		TAATATTTTG	TTAAAATTCG
2460		•	AGCTCATTTT		•	
2520			ACCGAGATAG			
2580			GACTCCAACG		,	
2640					GGGGTCGAGG	
2700	•		TCACCCTAAT			
2760	· .		GGGAGCCCCC			
2820			AAGAAAGCGA			
2880			ACCACCACAC		·	
2940			GGAAATGTGC		٠	•
3000			CTCATGAGAC			
3060			GCGGAAAGAA	·		
3120		,	CAGCAGGCAG			
3180	AGCAACCAGG	TGTGGAAAGT	CCCCAGGCTC	CCCAGCAGGC	AGAAGTATGC	AAAGCATGCA

53/56 F/G. 31. (CONTINUED)

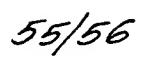
3240	•	TCAGCAACCA	TAGTCCCGCC	CCTAACTCCG	CCCATCCCGC	CCCTAACTCC
	GCCCAGTTCC	GCCCATTCTC	CGCCCCATGG	CTGACTAATT	TTTTTTATTT	ATGCAGAGGC
3300	CGAGGCCGCC	TCGGCCTCTG	AGCTATTCCA	GAAGTAGTGA	GGAGGCTTTT	TTGGAGGCCT
3360	• •	AAAGATCGAT	CAAGAGACAG	GATGAGGATC	GTTTCGCATG	ATTGAACAAG
3420	ATGGATTGCA	CGCAGGTTCT	CCGGCCGCTT	GGGTGGAGAG	GCTATTCGGC	TATGACTGGG
3480	CACAACAGAC	AATCGGCTGC	TCTGATGCCG	CCGTGTTCCG	GCTGTCAGCG	CAGGGGCGCC
3540		TGTCAAGACC				
3600	- - -			-		
3660		GTGGCTGGCC			• •	
3720	CTGAAGCGGG	AAGGGACTGG	CTGCTATTGG	GCGAAGTGCC	GGGGCAGGAT	CTCCTGTCAT
3780	-	TCCTGCCGAG	AAAGTATCCA	TCATGGCTGA	TGCAATGCGG	CGGCTGCATA
3840	CGCTTGATCC	GGCTACCTGC	CCATTCGACC	ACCAAGCGAA	ACATCGCATC	GAGCGAGCAC
3900	GTACTCGGAT	GGAAGCCGGT	CTTGTCGATC	AGGATGATCT	GGACGAAGAG	CATCAGGGGC
	Committee of the commit	CGAACTGTTC	GCCAGGCTCA	AGGCGAGCAT	GCCCGACGGC	GAGGATCTCG
3960	TCGTGACCCA	TGGCGATGCC	TGCTTGCCGA	ATATCATGGT.	GGAAAATGGC	CGCTTTTCTG
4020	GATTCATCGA	CTGTGGCCGG	CTGGGTGTGG	CGGACCGCTA	TCAGGACATA	GCGTTGGCTA
4080	CCCGTGATAT	TGCTGAAGAG	CTTGGCGGCG	AATGGGCTGA	CCGCTTCCTC	GTGCTTTACG
4140	GTATCGCCGC	TCCCGATTCG	CAGCGCATCG	CCTTCTATCG	CCTTCTTGAC	GAGTTCTTCT
4200	GAGCGGGACT	CTGGGGTTCG	AAATGACCGA	CCAAGCGACG	CCCAACCTGC	CATCACGAGA
4260						
4320	and the second	ACCGCCGCCT				
4380	CGGCTGGATG	ATCCTCCAGC	GCGGGGATCT	CATGCTGGAG	TTCTTCGCCC	ACCCTAGGGG
4440	GAGGCTAACT	GAAACACGGA	AGGAGACAAT	ACCGGAAGGA	ACCCGCGCTA	TGACGGCAAT
4500	AAAAAGACAG	AATAAAACGC	ACGGTGTTGG	GTCGTTTGTT	CATAAACGCG	GGGTTCGGTC
4560	CCAGGGCTGG	CACTCTGTCG	ATACCCCACC	GAGACCCCAT	TGGGGCCAAT	ACGCCCGCGT
4620	TTCTTCCTTT	TCCCCACCCC	ACCCCCAAG	TTCGGGTGAA	GGCCCAGGGC	TCGCAGCCAA
-	CGTCGGGGCG	GCAGGCCCTG	CCATAGCCTC	AGGTTACTCA	TATATACTTT	AGATTGATTT
4680	AAAACTTCAT	TTTTAATTTA	AAAGGATCTA	GGTGÄAGATC	CTTTTTGATA	ATCTCATGAC
4740	CAAAATCCCT	TAACGTGAGT	TTTCGTTCCA	CTGAGCGTCA	GACCCCGTAG	AAAAGATCAA
4800	AGGATCTTCT	TGAGATCCTT	TTTTTCTGCG	CGTAATCTGC	TGCTTGCAAA	CAAAAAAACC
4860			7 7 7		 	

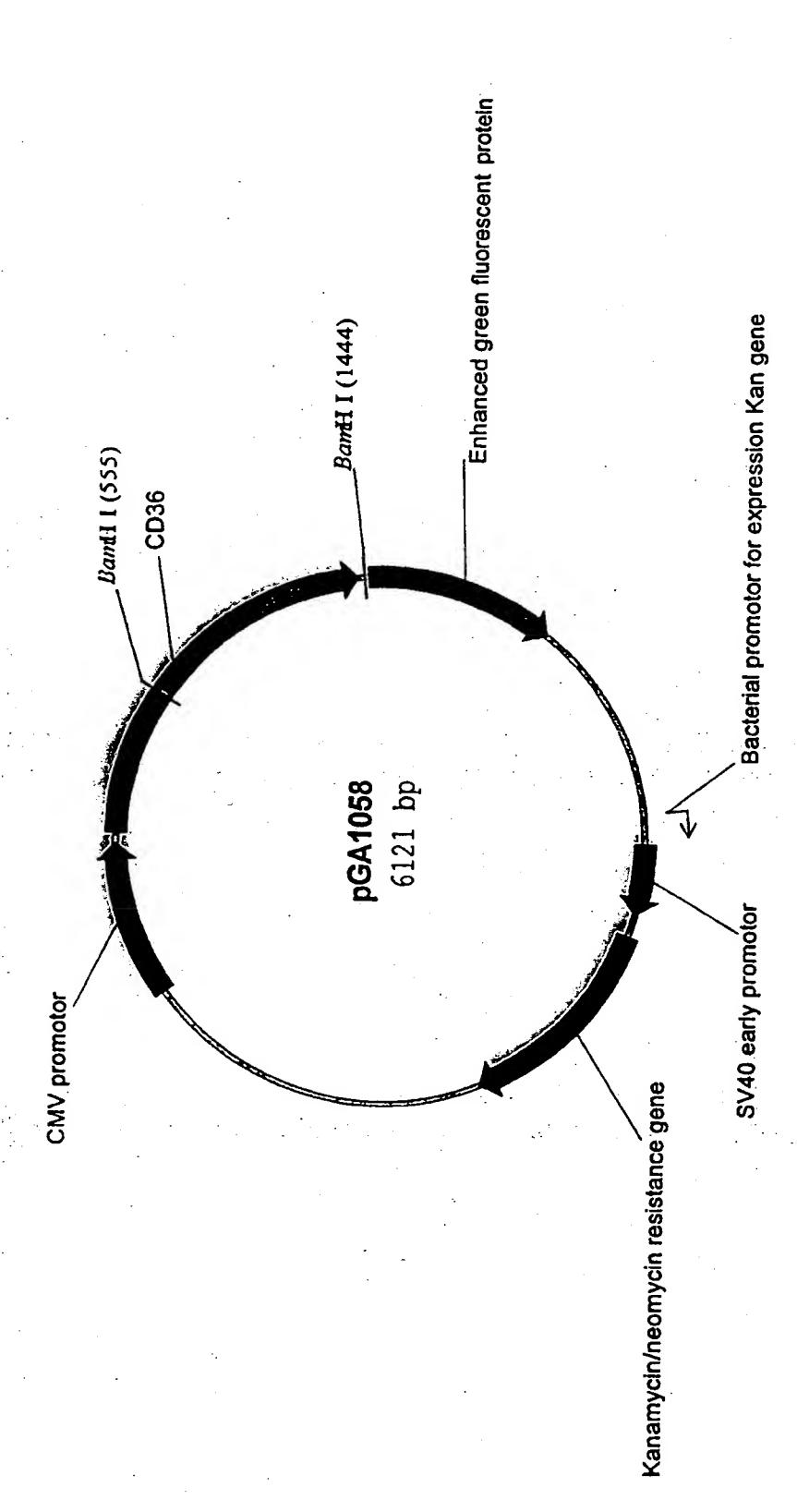
WO 99/64586

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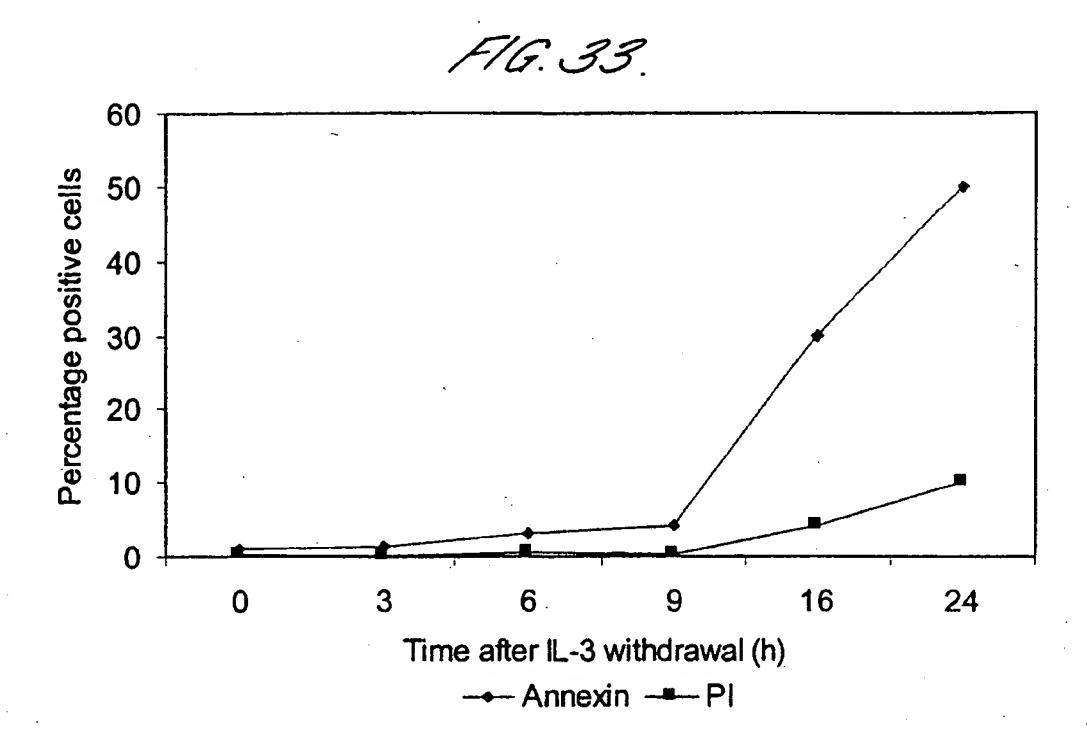
FIG. 31. (CONTINUED)

4000	ACCGCTACCA	GCGGTGGTTT	GTTTGCCGGA	TCAAGAGCTA	CCAACTCTTT	TTCCGAAGGT
4920	AACTGGCTTC	AGCAGAGCGC	AGATACCAAA	TACTGTCCTT	CTAGTGTAGC	CGTAGTTAGG
4980	CCACCACTTC	AAGAACTCTG	TAGCACCGCC	TACATACCTC	GCTCTGCTAA	TCCTGTTACC
5040	AGTGGCTGCT	GCCAGTGGCG	ATAAGTCGTG	TCTTACCGGG	TTGGACTCAA	GACGATAGTT
5100	ACCGGATAAG	GCGCAGCGGT	CGGGCTGAAC	GGGGGGTTCG	TGCACACAGC	CCAGCTTGGA
5160	GCGAACGACC	TACACCGAAC	TGAGATACCT	ACAGCGTGAG	CTATGAGAAA	GCGCCACGCT
5220	TCCCGAAGGG	AGAAAGGCGG	ACAGGTATCC	GGTAAGCGGC	AGGGTCGGAA	CAGGAGAGCG
5280	CACGAGGGAG	CTTCCAGGGG	GAAACGCCTG	GTATCTTTAT	AGTCCTGTCG	GGTTTCGCCA
5340	CCTCTGACTT	GAGCGTCGAT	TTTTGTGATG	CTCGTCAGGG	GGGCGGAGCC	TATGGAAAAA
5400	CGCCAGCAAC	GCGGCCTTTT	TACGGTTCCT	GGCCTTTTGC	TGGCCTTTTG	CTCACATGTT
5460	CTTTCCTGCG	TTATCCCCTG	ATTCTGTGGA	TAACCGTATT	ACCGCCATGC	ATTAGTTATT
5520	AATAGTAATC	AATTACGGGG	TCATTAGTTC	ATAGCCCATA	TATGGAGTTC	CGCGTTACAT
5580	AACTTACGGT	AAATGGCCCG	CCTGGCTGAC	CGCCCAACGA	CCCCGCCCA	TTGACGTCAA
5640	·	TGTTCCCATA				
5700	•	GTAAACTGCC				<u>.</u>
5760		CGTCAATGAC				
5820		TCCTACTTGG			·	
5880	•	GCAGTACATC		· · · · · · · · · · · · · · · · · · ·		
5940			·			
6000		CATTGACGTC				
6060		TAACAACTCC			•	
6120	٠	AAGCAGAGCT	GGTTTAGTGA	ACCGTCAGAT	CUGCTAGCGC	TACCGGACTC
6121	A				,	

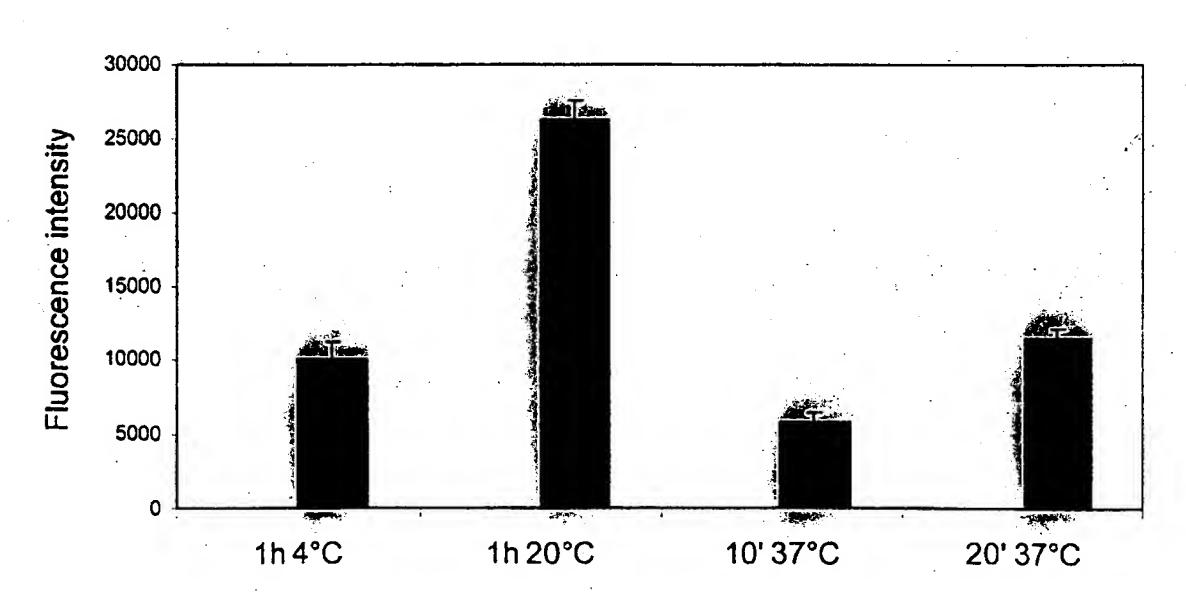




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F1G. 34.



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Thereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to:

Assistant Commissioner for Patents, Washington, D.C. 20231.

Typed or Printed Name

Donna Macedo.

Signature

Date

TOSK-004

SUPPLEMENTAL INFORMATION DISCLOSURE STATEMENT UNDER 37 C.F.R. § 1.97(e)

Address to: Assistant Commissioner for Patents Washington, D.C. 20231

Attorney Docket	TOSK-004				
First Named Inventor	FOGARTY, Patrick				
Application Number	09/472,654				
Filing Date	December 27, 1999				
Group Art Unit	1648				
Examiner Name	Unassigned				
Title	In Vivo High Throughput Toxicology Screening Method				

Sir:

Applicants submit herewith patents and/or publications which may be material to the examination of this application and in respect of which there may be a duty to disclose in accordance with 37 C.F.R. §1.56. While this Statement may be "material" pursuant to 37 C.F.R. §1.56, it is not intended to constitute an admission that any patent, publication, or other information referred to therein is "prior art" for this invention unless specifically designated as such. A listing of patents and/or publications is shown on enclosed Form PTO-1449 and a copy of each patent and/or publication is also enclosed.

Each item of information contained in the Information Disclosure Statement filed herewith was cited in a communication from a foreign patent office in a counterpart foreign application not more than three months prior to the filing of this Statement (37 C.F.R. 1.97(e)(1)). A copy of the communication is enclosed for the Examiner's convenience.

The Examiner is requested to make the citations listed on the enclosed PTO 1449 of record in this application. Applicants would appreciate the Examiner initialing and returning the initialed copy of form PTO 1449, indicating the references have been considered and made of record herein.

Atty Dkt. No.: TOSK-004

USSN: 09/472,654

No fee is believed due as this statement is being submitted within three months of the mailing date of the enclosed foreign communication. However, if it is determined that fees are required, the Commissioner is hereby authorized to charge any necessary fees associated with this communication or credit any overpayment to Deposit Account No. 50-0815.

Respectfully submitted, BOZICEVIC, FIELD & FRANCIS LLP

Date: 11.7.00

By: Bret E. Field

Registration No.37,620

BOZICEVIC, FIELD & FRANCIS LLP 200 Middlefield Road, Suite 200 Menlo Park, California 94025

Telephone: (650) 327-3400 Facsimile: (650) 327-3231

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